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PmagPy Cookbook

April 11, 2016

Dear Reader,

This documentation is updated from that in the book entitled *Essentials of Paleomagnetism* by Tauxe et al., (2010). This cookbook was designed as a companion website to the book Essentials of Paleomagnetism, 4th Web Edition. Chapter references to this companion book are, for example, “Essentials Chapter 1”.

There are many chefs who contributed to this work, in particular, the MagIC Database Team (Cathy Constable, Anthony Koppers, Rupert Minnett, Nick Jarboe, Ron Shaar, and Lori Jonestrask). Nick Swanson-Hysell (UC Berkeley) contributed the demag_gui and Jupyter notebook documentation. The PmagPy project is supported by grants from the National Science Foundation.

A pdf version of this cookbook is available for download at: PmagPy.pdf.

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Chapter 1

Installing PmagPy

You have a few options for downloading and using PmagPy. If you only want to try Pmag/Magic GUIs, you can download both of them as standalone programs. If you want full access to PmagPy functionality, you must first install the recommended version of Python. Then use the pip utility to download/install several PmagPy modules.

1.1 Standalone GUI download

If you do not need the full PmagPy functionality, and you only want to use Pmag GUI, MagIC GUI, Thellier GUI, and Demag GUI, there is now a standalone download for you. You won't need to install Python for this. You can download the standalone applications for OSX here, and for Windows here.

Follow the download instructions in the provided links, and then you can skip the “Full install” section and go straight to using Pmag GUI or MagIC GUI. The standalone versions of these applications are still in development; please report problems to the PmagPy team: ltauxe@ucsd.edu.

1.1.1 OSX Standalone download

To get started, download the zip file and put the resulting folder on your desktop. Inside the PmagPy-Standalone folder you will have one folder each for Pmag GUI and Magic GUI. Open the appropriate folder and double click the icon (depending on your security settings, you may have to right click the icon and then select “ok” the first time you open it).

You'll find the latest stable release at:

<https://github.com/PmagPy/PmagPy-Standalone-OSX/releases/latest>

1.1.2 Windows Standalone download

In order to install this software, you will need to download and install Microsoft Visual C++ Redistributable Package. This provides some back-end dependencies that let our software run.

Next, get started by downloading the zip file (see links below) and putting the resulting folder on your desktop. You'll need to "extract all" files. Inside the PmagPy-Standalone folder you will find icons for installing Pmag GUI and MagIC GUI. Double click the program you wish to use and you will be guided through the install process.

You'll find the latest stable release at:

<https://github.com/PmagPy/PmagPy-Standalone-Windows/releases/latest>

1.2 Full PmagPy install

To get the full use of PmagPy functionality, you will first have to install Python.

- Download and install the Enthought Canopy distribution of Python. Canopy Express (the free version) contains everything you need (except the mapping utilities). If you are at a degree-granting educational institution you can request an academic license that gives you access to additional features and bundled packages, including the Basemap package.
- Launch Canopy to complete the installation process. You may need to use control click on the Canopy icon to open it for the first time—try this if you get a message that says “Canopy can't be opened because it is from an unidentified developer.” Once you've opened Canopy successfully, select “yes” to making Canopy your default Python environment. In the lower right hand corner of the Canopy launch page, you will find the Version number (currently 1.6.1 or higher). Please include this in any correspondence with the PmagPy team. While you might find use for some of the features within the Canopy environment that opens as an application, PmagPy programs are best run or launched on the command line.
- Optional: Setting up Basemap for use in making maps with Python Once you have installed the full version of Canopy and want to use the mapping programs (e.g., basemap_magic.py), click on the ‘Package Manager’ button on the Canopy welcome page, and then on ‘Available

Packages’. Install both basemap packages (one has high resolution data files in it).

- A last note about Canopy: you should update it regularly! Open the Canopy application and update the packages at least every few months.

1.2.1 Installing PmagPy

Here we provide instructions for using pip to install PmagPy from the command line. “Pip” is a package manager that comes standard with any modern Python distribution (NB: you will have to update it to the most recent version). Pip allows you to install and uninstall pmagpy, the package with all the low-level functionality of PmagPy and pmagpy-cli which provides the PmagPy command-line-interface and has all the packages you may use to download/upload, visualize, and manipulate data.

To install using pip:

- Find and open your command line.
- Update pip: type on the command line:

```
pip install --upgrade pip
```

- Install or update pmagpy: use the command:

```
pip install --upgrade pmagpy
```

- Install or update pmagpy-cli, use the command:

```
pip install --upgrade pmagpy-cli
```

- To uninstall either, use the command: “pip uninstall pmagpy” or “pip uninstall pmagpy-cli”
- If you run into trouble, use pip to uninstall both pmagpy and pmagpy-cli, then try again to install first pmagpy and then pmagpy-cli

1.2.2 Finishing up

Now your installation should be complete. There are a few more details:

- Testing your installation:

To make sure everything is working, return to your command line (or PmagPy Prompt), type `eqarea.py -h`. Important note for Windows users: you will need to use “`eqarea -h`”. In fact, you will drop the “`.py`” anytime you are calling a command-line program.

If you do not see the help message, first try setting your path by hand following the instructions on the Trouble Shooting page. If that fails, please send the error message and Canopy version number to `ltauxe@ucsd.edu`

- Accessing example data files:

There are many data files used in the examples of programs and for use with the textbook Essentials of Paleomagnetism. You may want to copy the data files to your Desktop or another convenient location. To do this, navigate on the command line to your destination folder (for help, see this section). Then, use the command:

```
move_data_files.py -d .
```

This will copy all of the PmagPy example files to your current directory (represented by “`.`”).

- Installing the Etopo20 package for use with Basemap:

To install the Etopo20 package, see `install_etopo.py`.

1.3 Next steps

Where do you want to go from here?

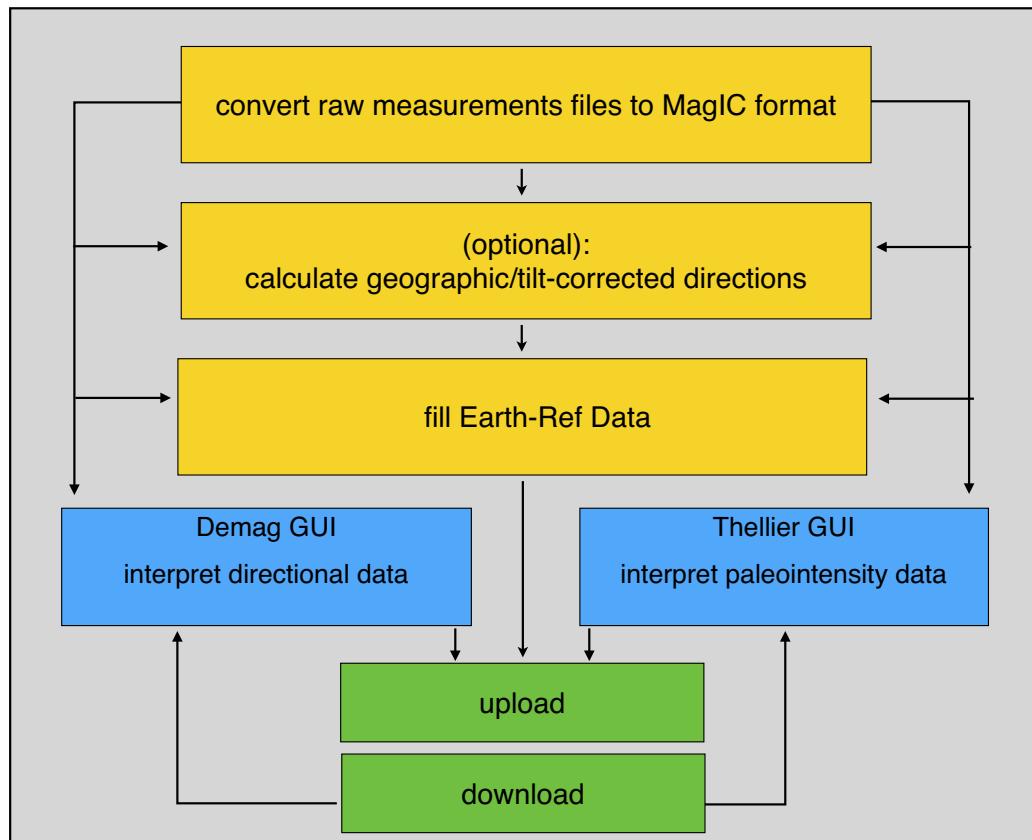
- Download data from the **MagIC** database.
- Analyze and/or upload demagnetization and/or paleointensity measurement data to the **MagIC** database.
- Learn more about particular programs in the **PmagPy** software package.
- Learn about the MagIC Database.

- Learn how to write your own programs in Python.
- Learn how to use Jupyter notebooks for managing your data analysis workflow.

Chapter 2

Pmag GUI Tutorial

Pmag GUI is a Graphical User Interface (GUI) written by Lori Jonestrask and Ron Shaar that provides a quick path to the main **PmagPy** programs. The work flow is illustrated schematically here:



1. Follow the steps in the Installing PmagPy section.
2. When you invoke **Pmag GUI**, the first step is to change directories into a ‘Project Directory’. For each study, create a directory with a name that relates to that study. Here we will call it *ThisProject*. This is where you will collect and process all the rock and paleomagnetic data for a given study, usually a publication. The project directory name should have NO SPACES and be placed on the hard drive in a place that has NO spaces in the path. Under certain Windows versions, this means you should not use your home directory, but create a directory called for example: D:\MyPmagProjects and put *ThisProject* there.
3. **copy example files:** In the *data_files* folder you will find a subfolder named *Pmag_GUI*. Copy the contents of the *ThisProject* directory into your own Project Directory folder.
4. Start Pmag GUI either by typing **pmag_gui.py** on your command line, or (if you have the standalone), by double-clicking the Pmag GUI icon on your Desktop.
5. Change directories by clicking on the “change dir” button and select your own *ThisProject* directory.

2.1 Converting magnetometer files to MagIC format

- **Pmag GUI** allows for converting many different laboratory formats. For the complete set of instructions, see the section on Supported Rock Magnetometer files. For this example, we will use a ‘generic’ file format. An example for a generic file format is shown here:

	A	B	C	D	E	F	G	H	I	J
Sheets	Charts	SmartArt Graphics	WordArt							
1 specimen	treatment	treatment_type	moment	dec_s	inc_s	dec_g	inc_g	dec_t	inc_t	
2 sr01e2		0 A	2.93E-02	200.6	27.9					
3 sr01e2		10 A	2.83E-02	201	27.7					
4 sr01e2		20 A	2.61E-02	200.5	27.4					

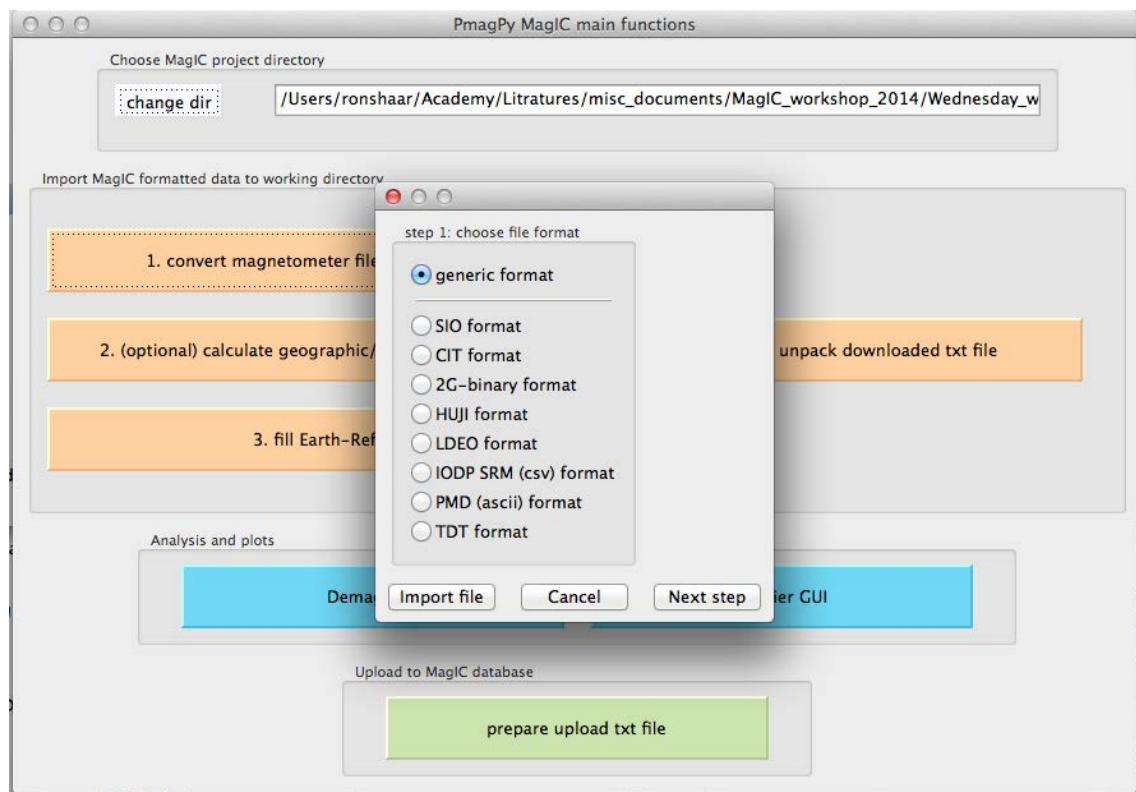
To learn what all the column headers mean look at the documentation for *generic_magic.py*.

- In your *ThisProject* directory there are three files with AF, Thermal, and Thellier measurement data of specimens from site sr01 (a lava flow

2.1. CONVERTING MAGNETOMETER FILES TO MAGIC FORMAT11

site) of Tauxe et al. (2004). There is also a file with sample orientation, location and other metadata typical for a paleomagnetic study.

- Press the [Convert magnetometer files to MagIC format] button. If no menu pops up or the window is blank, click on the Python icon (the little space ship) on your dock. You should see a dialog window will appear with different file formats:



- Click on ‘generic format’ and press the [import file] button. A new dialog box will appear. For more details click on the [help] button.
- In the dialog box, click on the [Add] button and choose one of the measurements files.
- Optional: Insert your EarthRef user name.
- Choose your experiment type from the dropdown list.
- Choose specimen-sample naming convention. In this example, specimen sr01a1 belongs to sample sr01a so the specimen-sample naming

convention is ‘no. of terminal characters’ and the delimiter/number field is ‘1’).

- Choose sample-site naming convention. In this example, sample sr01a belongs to site sr01 so the sample-site naming convention is ‘no. of terminal characters’ with a delimiter/number of ‘1’.

- Fill in the EarthRef Location Name for this project . For this project, it is “Snake River”.

- Note: a location is a stratigraphic section, a sampling region, an drill core, and so on. MagIC doesn’t really care what your location name is, but use the same location name every time you are asked for it, because it really ties your dataset together and is required within the data model.

Your dialog boxes should look like this for the AF and thermal data:

2.1. CONVERTING MAGNETOMETER FILES TO MAGIC FORMAT13

For AF or thermal demagnetization data

PmagPy generic file conversion

convert generic file to MagIC format

Choose file (no spaces are allowed in path):
 /Users/ronshaar/Academy/Litratures/misc_documents/MagIC

User name (optional): rshaar

Experiment: Demag (AF and/or Thermal)

Lab field (leave blank if unnecessary). Example: 40 0 -90
B (uT) dec inc

specimen-sample naming convention delimiter/number (if necessary)
no. of terminal characters 1

sample-site naming convention delimiter/number (if necessary)
no. of terminal characters 1

Location name: Snake River

replicate measurements:
 Average replicate measurements
 take only last measurement from replicate measurements

and like this for the paleointensity data. For paleointensity data, you must also supply the lab field in micro tesla (40) and orientation relative to sample's X direction: 0 90.

2.1. CONVERTING MAGNETOMETER FILES TO MAGIC FORMAT15

Paleointensity data

PmagPy generic file conversion

convert generic file to MagIC format

Choose file (no spaces are allowed in path):
 /Users/ronshaar/Academy/Litratures/misc_documents/MagIC

User name (optional): rshaar

Experiment: Paleointensity-IZZI/ZI/ZI

Lab field (leave blank if unnecessary). Example: 40 0 -90
B (uT) dec inc
40 0 90

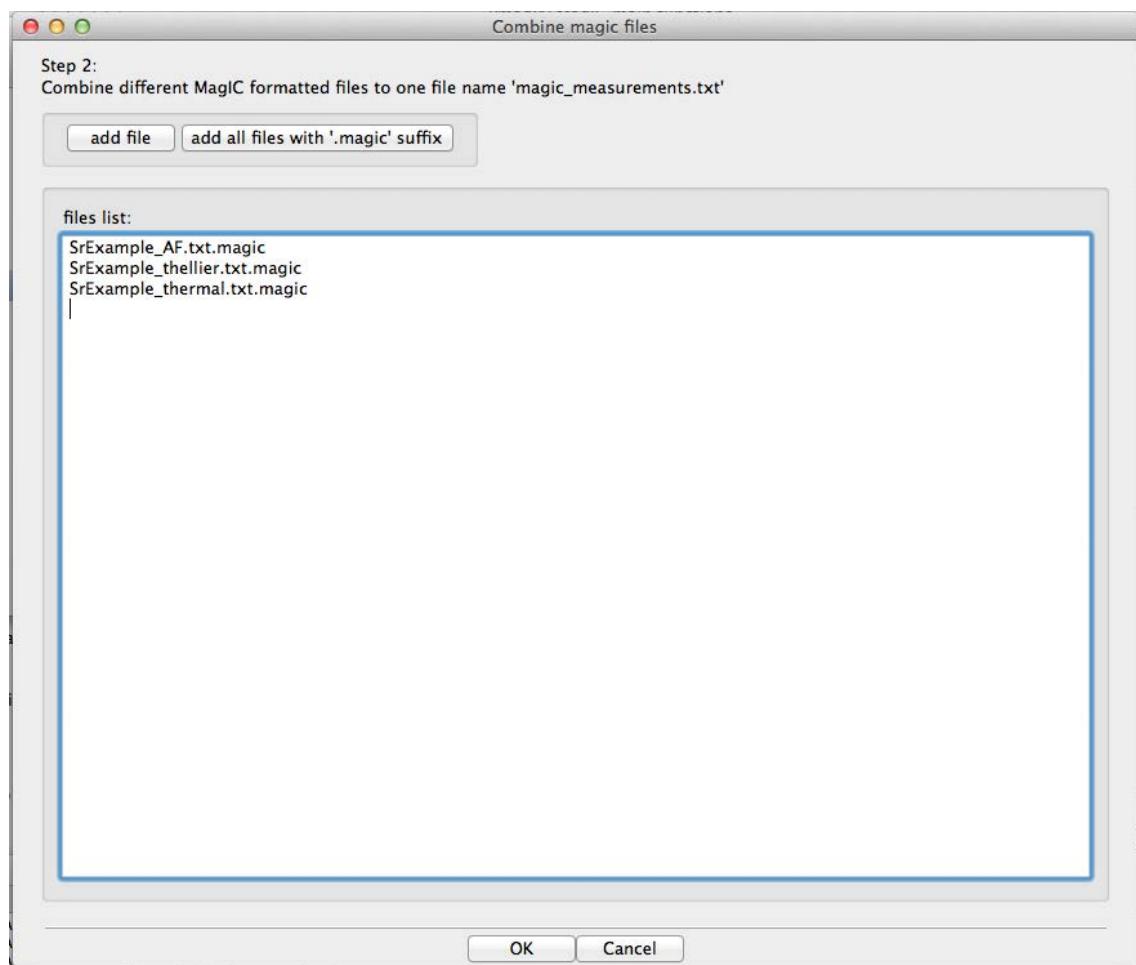
specimen-sample naming convention delimiter/number (if necessary)
no. of terminal characters ▾ 1

sample-site naming convention delimiter/number (if necessary)
no. of terminal characters ▾ 1

Location name: Snake River

replicate measurements:
 Average replicate measurements
 take only last measurement from replicate measurements

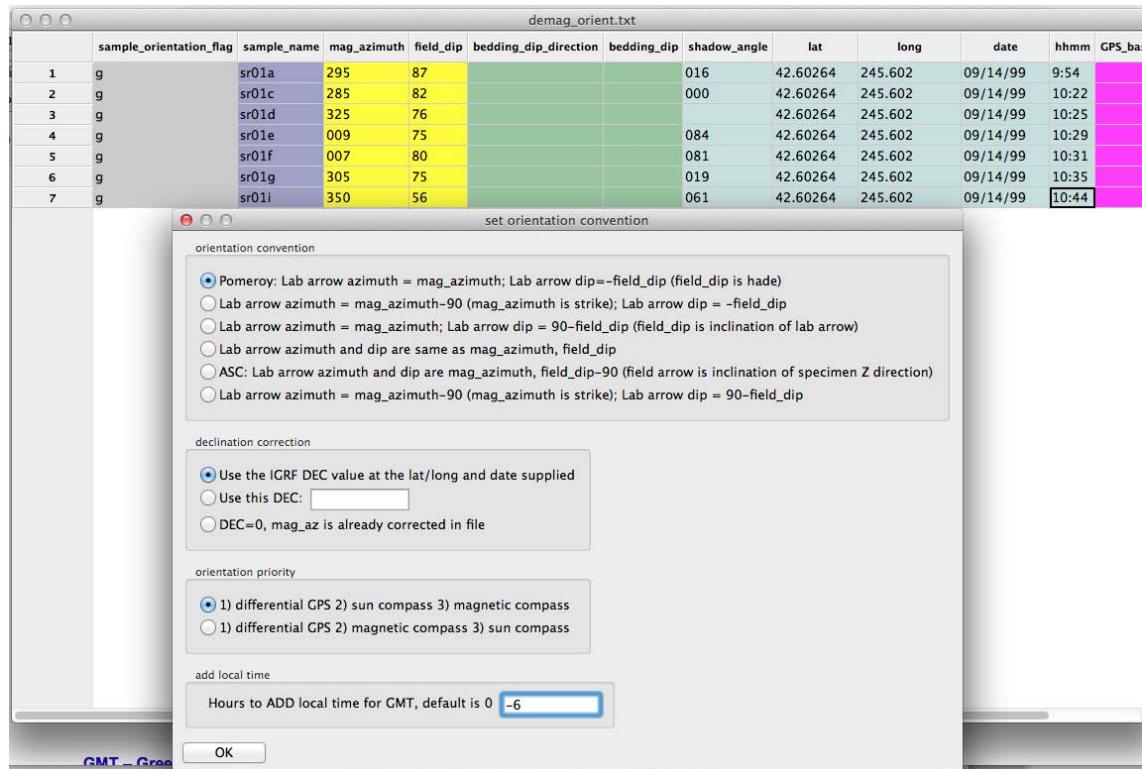
- Press OK to create a new MagIC measurement file, which is saved in your *ThisProject* directory.
- After converting all files to MagIC format, press the [Next Step] button in the ‘convert magnetometer files’ dialog box. All files with the .magic suffix will be added to the list. [You can edit the list by deleting unwanted files or adding additional MagIC formatted files.] You should see a list of the three magic files:



- Click the OK button. The three files will be combined to a single file, named *magic-measurements.txt* and also stored in your *ThisProject* directory.

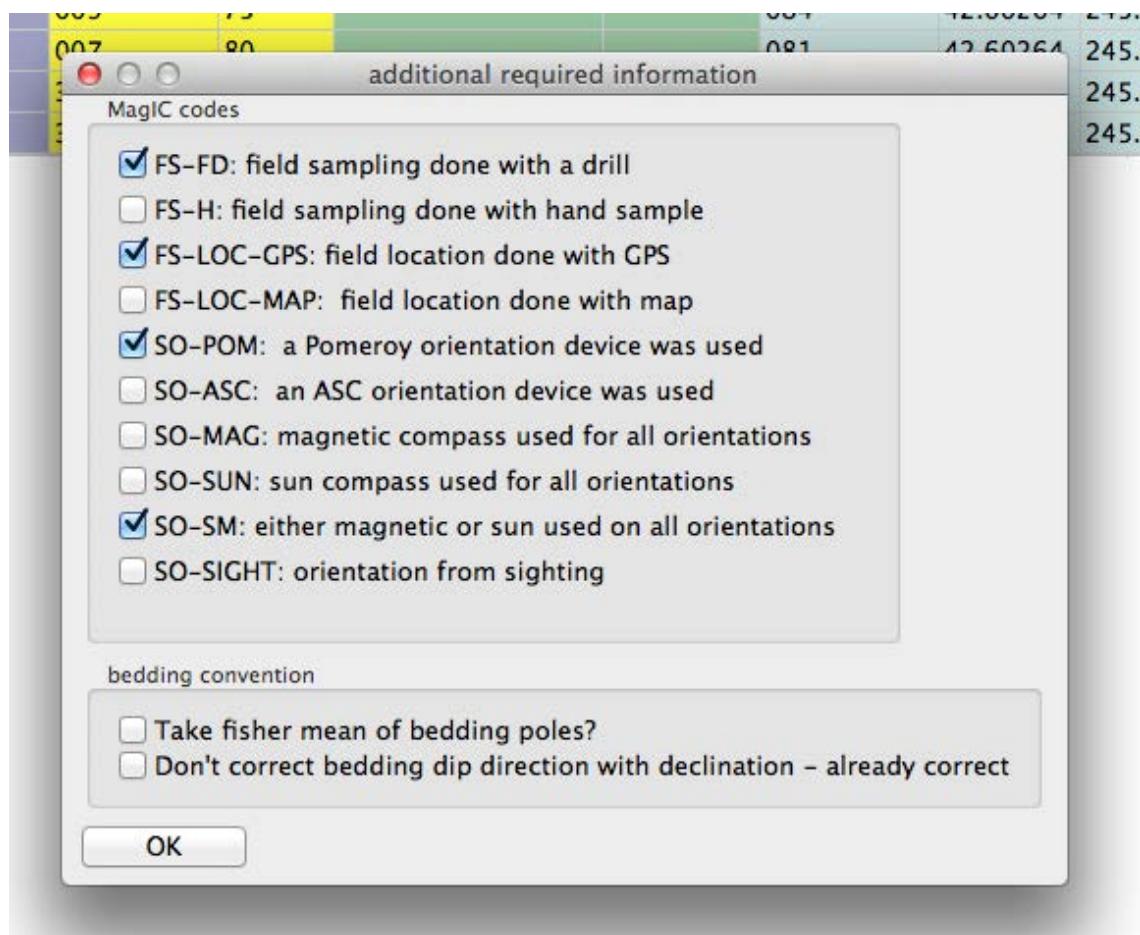
2.2 Optional: Calculate geographic / tilt-corrected direction

- **Pmag GUI** provides an optional tool for calculating geographic and tilt-corrected directions if those directions were not part of the original data files. To use this tool click on the button labeled ‘calculate geographic/tilt-corrected directions’.
- An empty template of a file named SrExample_orient.txt was created in the MagIC Project Directory. This file is displayed in a Python window. You can fill in this file manually using the Python window or with a spreadsheet program (recommended). The empty template has now only the sample names derived from your measurement files, using the naming rules that you chose.
- To see an example of a filled in one, pull down the menu bar [file] → [open orientation file] and choose the file SrExample_orient.txt from *MyFiles* folder.
- Choose from the menu bar [file] → [Save orientation file].
- Choose from the menu bar [file] → [Calculate sample orientation].
- Fill in the dialog box like this:



- Orientation convention :Pomeroy.
- Declination correction: Use the IGRF.
- Orientation priority: #1.
- Put in the number of hours to SUBTRACT from the local time to get to Greenwich Mean Time: -6. [Local time was 6 hours behind GMT for this example.]
- press the OK button.

- In the next dialog window add the additional information:

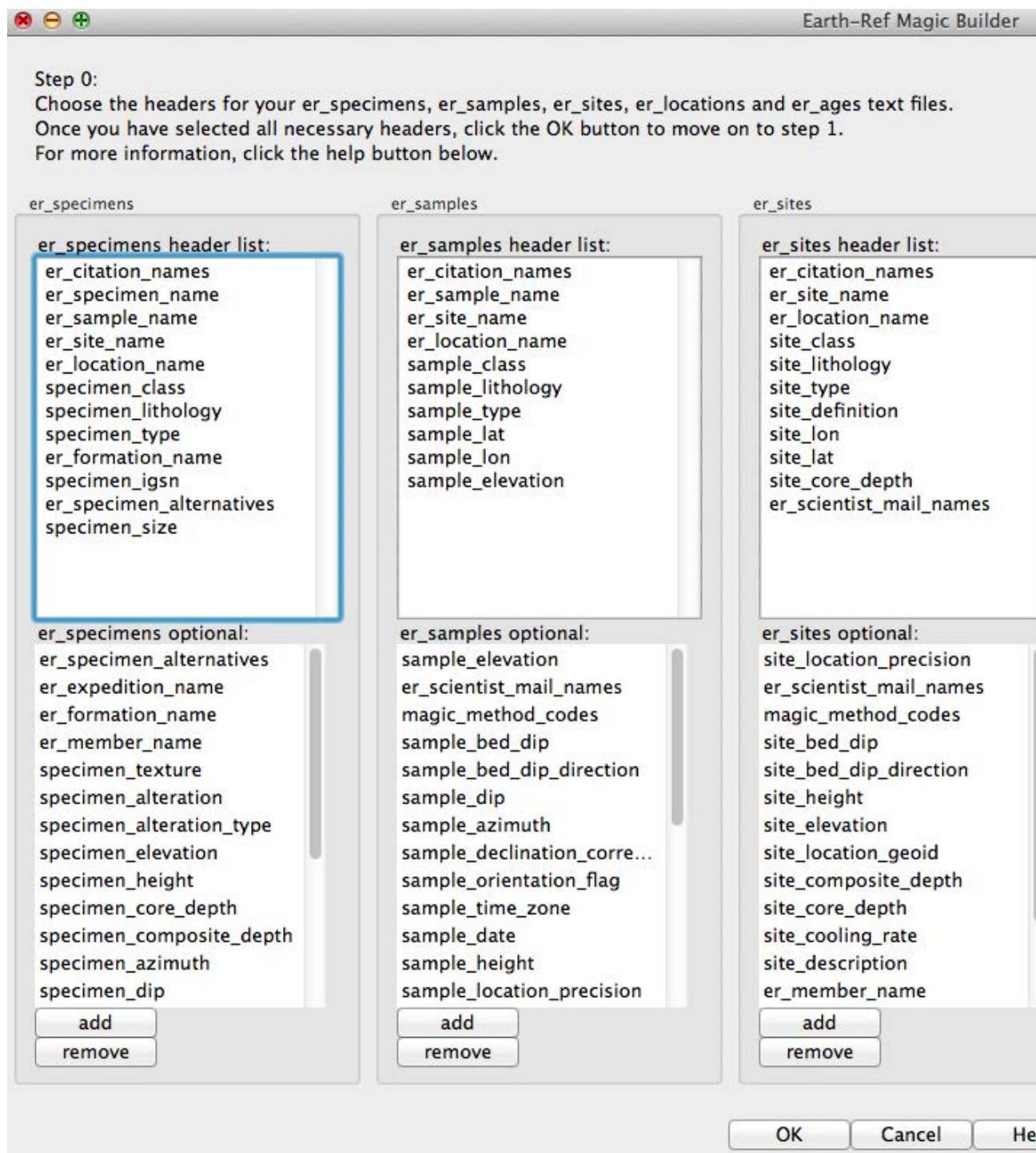


2.3 Filling in the EarthRef data

Filling in the Earth Ref data is a critical part of building a MagIC Project Directory. The Earth-Ref data relevant to this example are arranged in five er_* tables: er_specimens, er_samples, er_sites, er_locations, er_ages. To complete the ER data, click the button, and follow the directions in the help window in order:

- Step 0: Choose the appropriate headers for each of your er_* tables. Required headers (or headers already present in your er_* tables) show up in the top box, optional headers in the bottom. In our example, the only header you should add is “age_sigma” in the age table. Once

you have added all needed headers, click the OK button to proceed to the next step.



- The next six steps contain editable grids. For many columns, you can edit using drop-down menus that provide controlled vocabularies. For others, you must manually enter data into the cell. A single left click will bring up a drop-down menu; a double-left click will call up the cell editor. With both types of data entry, it is possible to select a single value for the entire column. Simply click on the column label. If that column has a drop-down menu, you can then click on any cell in the column, the appropriate menu will pop up, and the value you select will propagate throughout the column. Edits in that column will continue to be global until you select another column to edit or you de-select the column by clicking on the column label again. If you select a column that does not have a drop-down menu, a text entry dialog will pop up, and the value you provide will be applied to the column.
- Step 1: Update the relationship between specimens and samples. You may not rename specimens, but you may reassign them to a different sample. It is also possible to add additional samples, using the 'Add new sample' button. Note that specimen_type, specimen_lithology, and specimen_class columns do not show up. They will propagate down when you select sample_type, sample_lithology, and sample_class in step 4.

The screenshot shows a software window titled "Check Data". At the top, there are three colored window control buttons (red, yellow, green) on the left and the title "Check Data" on the right. Below the title is a status message: "Step 1: Check that all specimens belong to the correct sample (if sample name is simply wrong, that will be fixed in step 2)". Underneath this message are four buttons: "Add a new sample", "Help", "Save", "Cancel", and "Save and continue". Below these buttons is a link "Delete selected row(s)". The main area of the window is a grid table with 8 rows and 7 columns. The columns are labeled: "er_specimen_name", "er_sample_name", "er_citation_names", "specimen_class**", "specimen_lithology**", and "specimen_type**". The first column contains numerical IDs from 1 to 8. The second column contains specimen names like "sr01a1", "sr01a2", etc. The third column contains sample names like "sr01a", "sr01c", etc. The fourth column contains citation names like "This study". The last three columns are empty. The "er_specimen_name" column is currently selected, as indicated by a black border around the first cell.

	er_specimen_name	er_sample_name	er_citation_names	specimen_class**	specimen_lithology**	specimen_type**
1	sr01a1	sr01a	This study			
2	sr01a2	sr01a	This study			
3	sr01c2	sr01c	This study			
4	sr01d1	sr01d	This study			
5	sr01e2	sr01e	This study			
6	sr01f2	sr01f	This study			
7	sr01g2	sr01g	This study			
8	sr01i1	sr01i	This study			

- Step 2: Update the relationship between samples and sites. You may rename samples, or you can reassign them to a different site. You can also add additional sites using the "Add a new site" button. You will

be able to update other columns in the er_samples file in step 4.

Check Data

Step 2:
Check that all samples are correctly named,
and that they belong to the correct site
(if site name is simply wrong, that will be fixed in step 3)

[Add a new site](#) [Help](#)

[Save](#) [Cancel](#) [Save and continue](#) [Back](#)

[Delete selected row\(s\)](#)

	er_sample_name	er_site_name
1	sr01a	sr01
2	sr01c	sr01
3	sr01d	sr01
4	sr01e	sr01
5	sr01f	sr01
6	sr01g	sr01
7	sr01i	sr01

- Step 3: Update the relationship between sites and locations. You may rename sites, or you can reassign them to a different location. You can add additional locations using the “Add a new location” button. You must choose a legal entry from the controlled vocabularies for the following headers: “site_class”, “site_lithology”, “site_type”. You may combine more than one controlled vocabulary by making them a colon delimited list. If you select a value in these categories:

class, lithology, type, longitude, or latitude, the values will propagate to the samples table. In this example, site_class=Extrusive:Igneous; site_lithology=Basaltic Lava; site_type=Lava Flow

Step 3:
 Check that all sites are correctly named, and that
 Fill in the additional columns with controlled vocabulary.
 The columns for class, lithology, and type can be
 You may use the drop-down menus to add as needed
 (see the help button for more details)
 note: Changes to site_class, site_lithology, or site_type
 However, you will be able to edit sample_class

**Denotes controlled vocabulary

	er_site_name	er_location_name	er_citation_names	site_class
1	sr01	Snake River	This study	Extrusive:Igneous

- Step 4: Some data from sites in Step 3 have propagated into the samples table. You may update and fill in all columns in the samples table here.

Step 4:
 Some of the data from the er_sites table has propagated into er_samples.
 Check that this data is correct, and fill in missing cells using controlled vocabularies.
 The columns for class, lithology, and type can take multiple values in the form of a colon-delimited list.
 You may use the drop-down menus to add as many values as needed in these columns.
 (see Help button for more details)

** Denotes controlled vocabulary

Add a new site	Help
Save	Cancel
Save and continue	
Back	
Delete selected row(s)	

	er_sample_name	er_site_name	er_citation_names	sample_class**	sample_lithology
1	sr01a	sr01	This study	Extrusive:Igneous	Basaltic Lava
2	sr01c	sr01	This study	Extrusive:Igneous	Basaltic Lava
3	sr01d	sr01	This study	Extrusive:Igneous	Basaltic Lava
4	sr01e	sr01	This study	Extrusive:Igneous	Basaltic Lava
5	sr01f	sr01	This study	Extrusive:Igneous	Basaltic Lava
6	sr01g	sr01	This study	Extrusive:Igneous	Basaltic Lava
7	sr01i	sr01	This study	Extrusive:Igneous	Basaltic Lava

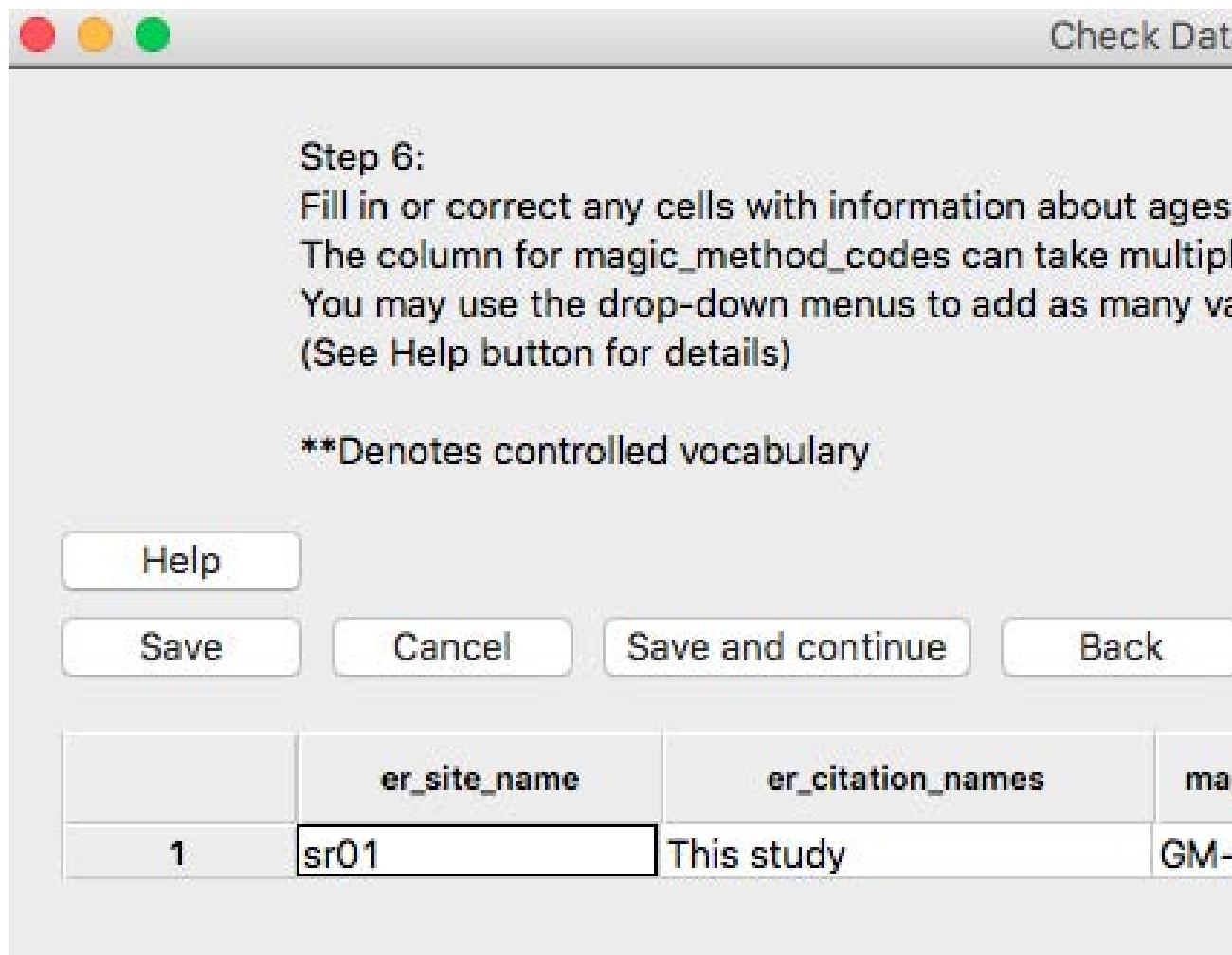
- Step 5: Fill in information for locations. If you have provided site latitudes and longitudes, the columns for beginning and ending latitudes and longitudes should be filled in already. You must choose a legal entry from the controlled vocabularies for the “location_type”. In this example: location_type = outcrop.

Step 5:
Check that locations
Fill in any blank cells
(See Help button for
more information)

** Denotes controlled vocabulary

Help	Save	Cancel	Save and continue	Back
Delete selected row(s)				
	er_location_name	er_citation_names	location_type**	
1	Snake River	This study	Outcrop	42.6

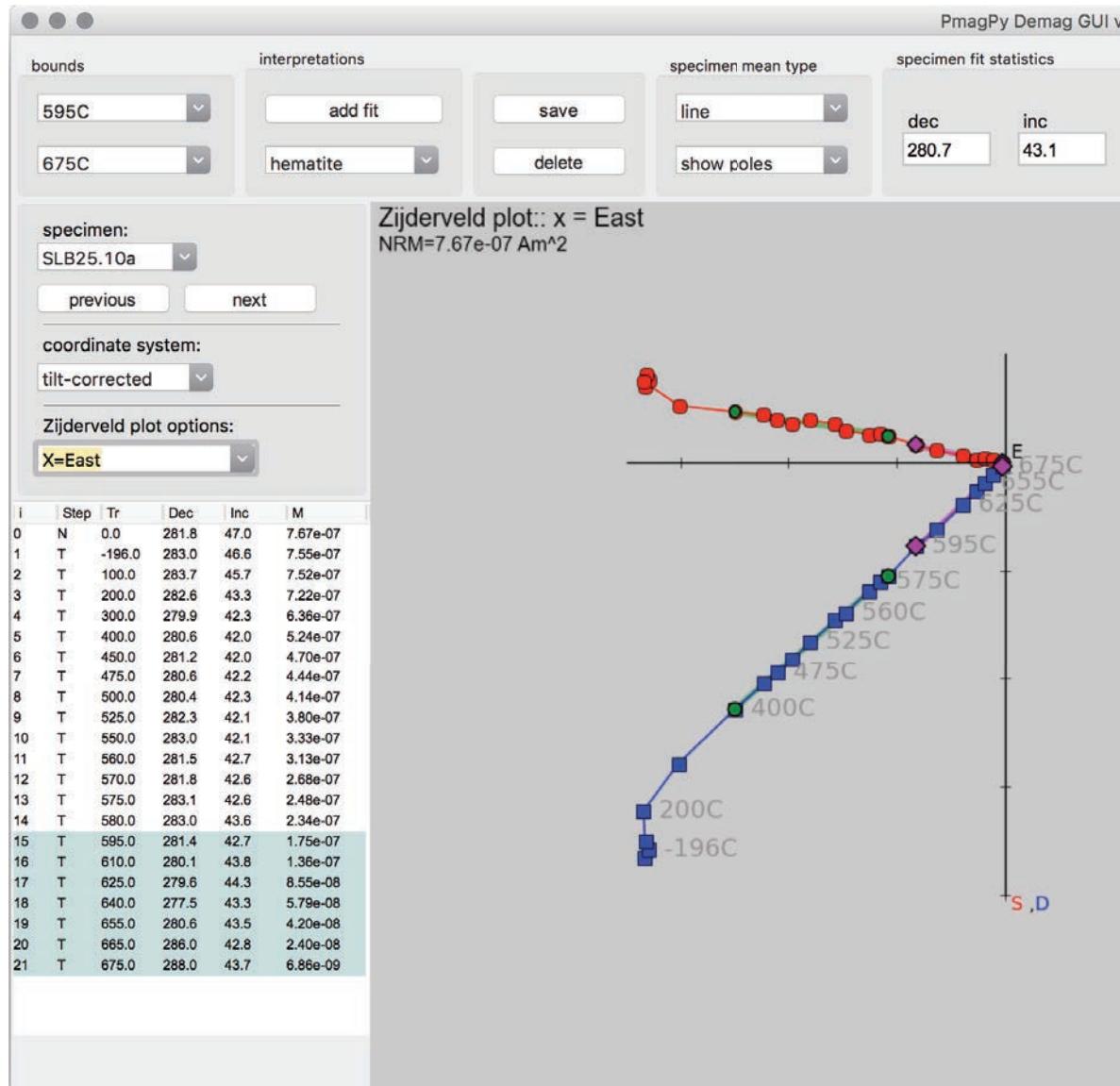
- Step 6: Fill in columns with any necessary information. In this example, age=3.4; age_sigma=0.03 (not a default header); age_unit=Ma (from controlled vocabularies), magic_method_codes = GM-ARAR-AP (from controlled vocabularies). It means “40Ar/39Ar age determination: Age plateau.”



- Note that if you re-run this sequence, certain values may be changed or overwritten. For example, if you set sample_lithology to be something different from site_lithology, re-running ErMagic will cause sample_lithology to revert back to being the same as site_lithology.
- You are now ready to move on to making some interpretations!

2.4 Demag GUI quick start

This image shows the main panel of the demag GUI:



Use of the Demag GUI is described in more detail in the Demag GUI section below. Here are a few instructions that can be used as a quick start for using Demag GUI.

To analyze the data in the example, follow these steps for each specimen:

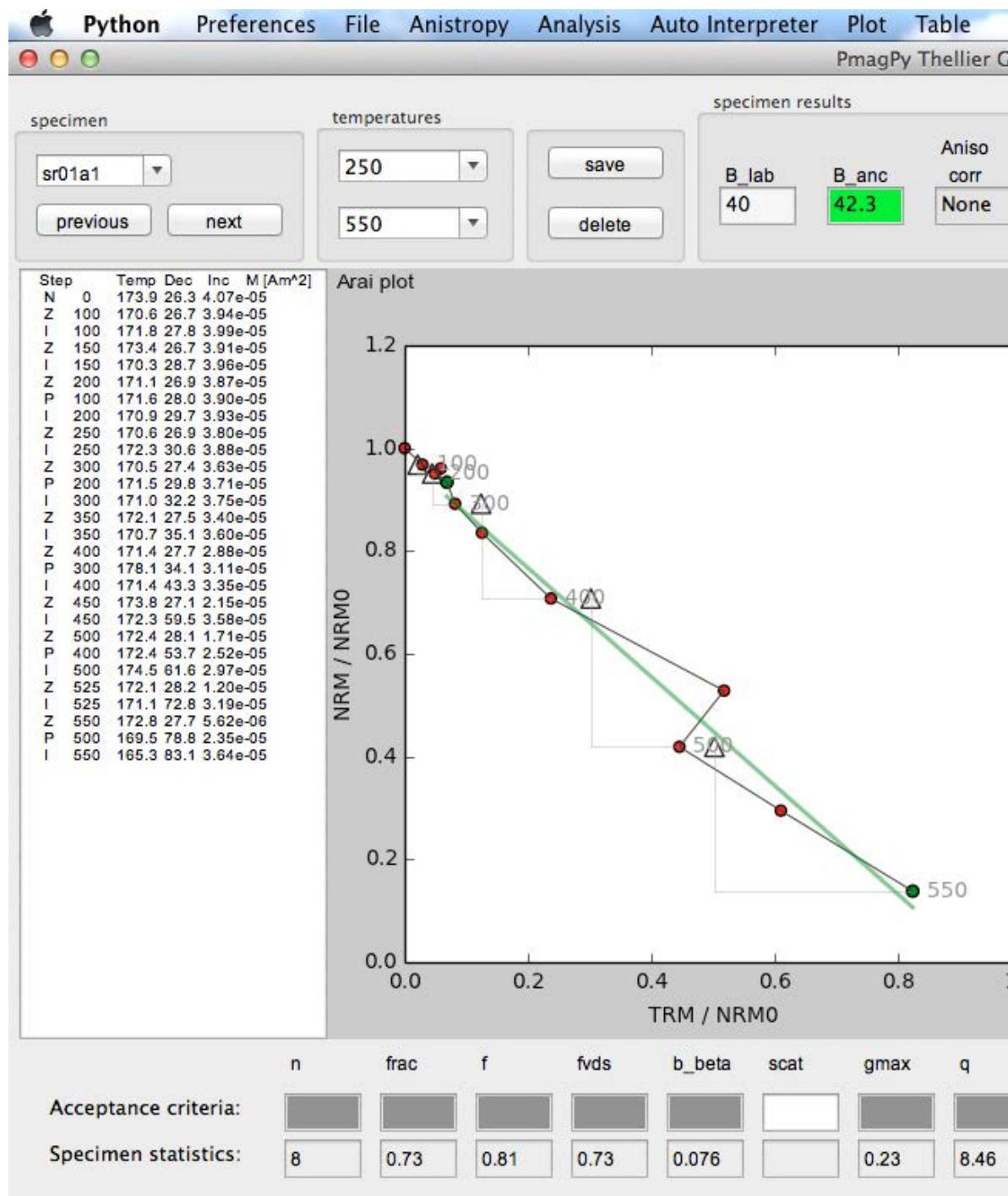
- From the ‘coordinate system’ drop-down menu you can choose the coordinate system in which you wish to view the data (e.g. ‘geographic’).
- Click ‘add a fit’ and choose the temperature/AF bounds for the fit

by double clicking on the measurement lines or by choosing from the ‘bounds’ dropdown menu.

- Click the ‘next’ button to analyze the next specimen.
- To calculate Fisher mean for the site: choose from the ‘higher level mean’ drop-down menus: show=specimens; mean=Fisher.
- All of the fits can be viewed and modified using the Interpretation Editor which can be selected from the Tools menu in the top menubar.
- To save all of the specimen interpretations, choose from the menubar [File] → [Save MagIC pmag tables]. This saves all the interpretations in MagIC formatted pmag-* files in your *ThisProject* directory. Fits that are saved this way will be loaded into demag-gui the next time it is launched.
- Click through the dialog boxes and fill out choices for the MagIC results table.
- Close the Demag GUI.

2.5 Thellier GUI quick start

This image shows the main panel of Thellier GUI:



Use of the Thellier GUI is described in more detail in the Thellier GUI section below and in this PDF document: Thellier GUI manual. Here are a few instructions that can be used as a quick start for using Thellier GUI.

To analyze the data in the example, follow these steps for each specimen:

- Choose temperature bounds from the temperatures dropdown menus.
- Click ‘save’ so the program remembers the interpretations (the interpretation is not saved to a file yet!).
- Click the ‘next’ button to analyze the next specimen.
- The default of the program is to calculate sample means. To change it to site level mean, choose from the menubar: [Analysis → [Acceptance criteria] → [Change acceptance criteria]. Find the ‘average by sample/site’ dropdown menu in the third row and change it to [site]. Click OK. The site mean will appear in the sample/site results box (top right).
- After all specimen interpretations are saved in memory, choose from the menubar [File] → [Save MagIC pmag tables]. This save all the interpretations in MagIC formatted pmag-* files in the MagIC Project Directory.
- Close the Thellier GUI.

2.6 Upload to the database

For this, you first click on the green *prepare upload txt file* button on the main page of **Pmag GUI**. A file named ‘upload.txt’ will be created in your *ThisProject* directory. Now, go to the MagIC search interface. Click on the ‘create’ button and find or create your reference.

Click on ‘Upload’ in the Actions column and drag and drop the *upload.txt* file onto the ‘Drop a MagIC Text File’ window. Congratulations. Your data are now in the database. But, they are not yet activated which you can do by clicking on the ‘Activate’ button in the Actions column. Once you activate an uploaded dataset (only for published papers), it will be publicly available.

2.7 Downloading data from MagIC

Data can be downloaded from the **MagIC** database and examined with **PmagPy** tools. The **MagIC** search interface provides a rich variety of search filters available by clicking on the ‘Filter the MagIC Search Results’ text box. To locate data from a particular reference, simply substitute the digital object identifier (DOI) in your browser window:

<http://earthref.org/MAGIC/doi/10.1029/2003GC000661>

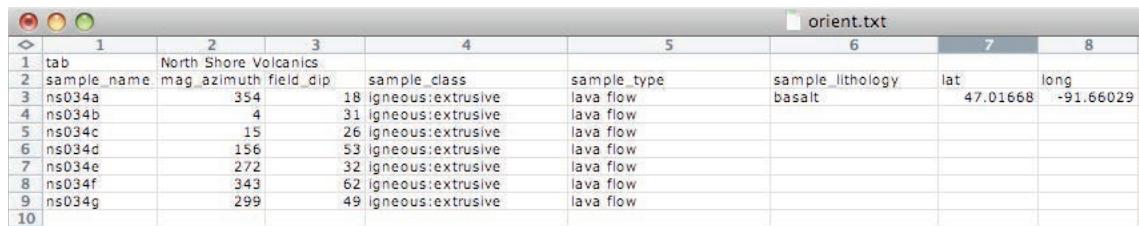
The above DOI will find the data for the paper by Tauxe et al. (2004). [This may fail in Safari; if so, use an alternative browser like Firefox or Chrome.] To download the data, simply click on the file icon below the column labeled ‘data’. This will save a file to your downloads folder. To unpack this file after downloading it from the database click the “unpack downloaded txt file button” in the Pmag GUI panel.

2.8 Preparing for MagIC

2.8.1 Field and sampling information

There is an astounding number of different ways that paleomagnetists document data in the field and in the lab. This variety is met with a large number of method codes that describe sampling and orientation procedures (see <http://earthref.org/MAGIC/methods.htm> for a complete description). The MagIC database expects sample orientations to be the azimuth and plunge of the fiducial arrow used for measurement (see [Essentials, Chapter 9]) and the orientation of the bedding to be dip direction and downward dip so no matter what your own preference is, it must be translated into the standard MagIC convention for use with the PmagPy programs and with Pmag GUI.

Pmag GUI supports two different ways of getting orientation and other sampling related information into a MagIC usable format. The first way is through step 2 on the GUI front panel and filling in the data from within the GUI. That way will work for many applications, but it may be desirable to fill the spreadsheet in separately from the GUI by using a tab delimited file (*orient.txt* format). By clicking on step 2 on the GUI front panel you create a file named *demag_orient.txt* which has all of your sample names in it. Each *orient.txt* file should have all the information for a single location *sensu MagIC*.



The screenshot shows a Microsoft Excel spreadsheet with the title bar 'orient.txt'. The data is organized into columns labeled 1 through 8. Column 1 contains sample names: ns034a, ns034b, ns034c, ns034d, ns034e, ns034f, and ns034g. Columns 2, 3, and 4 contain numerical values: mag_azimuth (354, 4, 15, 156, 272, 343, 299), field_dip (18, 31, 26, 53, 32, 62, 49), and date (354, 4, 15, 156, 272, 343, 299). Columns 5, 6, and 7 contain categorical data: sample_type (lava flow, lava flow, lava flow, lava flow, lava flow, lava flow, lava flow), sample_lithology (basalt, basalt, basalt, basalt, basalt, basalt, basalt), and GPS_Az (47.01668, -91.66029, -91.66029, -91.66029, -91.66029, -91.66029, -91.66029). Column 8 is empty.

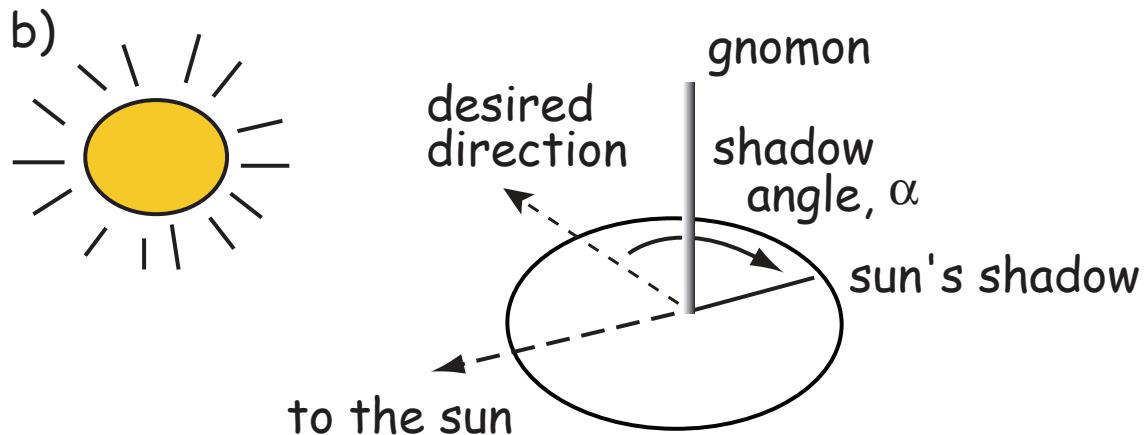
	1	2	3	4	5	6	7	8
1	tab	North Shore Volcanics						
2	sample_name	mag_azimuth	field_dip	sample_class	sample_type	sample_lithology	lat	long
3	ns034a	354	18	igneous:extrusive	lava flow	basalt	47.01668	-91.66029
4	ns034b	4	31	igneous:extrusive	lava flow			
5	ns034c	15	26	igneous:extrusive	lava flow			
6	ns034d	156	53	igneous:extrusive	lava flow			
7	ns034e	272	32	igneous:extrusive	lava flow			
8	ns034f	343	62	igneous:extrusive	lava flow			
9	ns034g	299	49	igneous:extrusive	lava flow			
10								

The next row has the names of the columns. The required columns are: sample_name, mag_azimuth, field_dip, date, lat, long, sample_lithology, sample_type, sample_class) but there are a number of other possible columns (e.g., Optional Fields in orient.txt formatted files are: [date, shadow_angle, hhmm], date, stratigraphic_height, [bedding_dip_direction, bedding_dip], [image_name, image_look, image_photographer], participants, method_codes, site_name, and site_description, GPS_Az]). Column names in brackets must be supplied together and the data for stratigraphic_height are in meters. Also note that if these are unoriented samples, just set mag_azimuth and field_dip to 0.

It is handy to document the lithology, type and material classification information required by MagIC. These are all controlled vocabularies listed at <http://earthref.org/MAGIC/shortlists.htm>. For archaeological materials, set the lithology to “Not Specified”.

Put in stratigraphic height, sun compass, differential GPS orientation information under the appropriate column headings. You can also flag a particular sample orientation as suspect, by having a column 'sample_flag' and setting it to either 'g' for good or 'b' for bad. Other options include documenting digital field photograph names and who was involved with the sampling.

For Sun Compass measurements, supply the shadow_angle, date and time. The date must be in mm/dd/yy format. If you enter the time in local time, be sure you know the offset to Universal Time as you will have to supply that when you import the file. Also, only put data from one time zone in a single file. The shadow angle should follow the convention shown in this figure (from Tauxe et al., 2010):



Supported sample orientation schemes:

There are options for different orientation conventions (drill direction with the Pomeroy orientation device [drill azimuth and hade] is the default), different naming conventions and a choice of whether to automatically calculate the IGRF value for magnetic declination correction, supply your own or ignore the correction. The program generates *er_samples.txt* and *er_sites.txt* files. Be warned that existing files with these names will be overwritten.

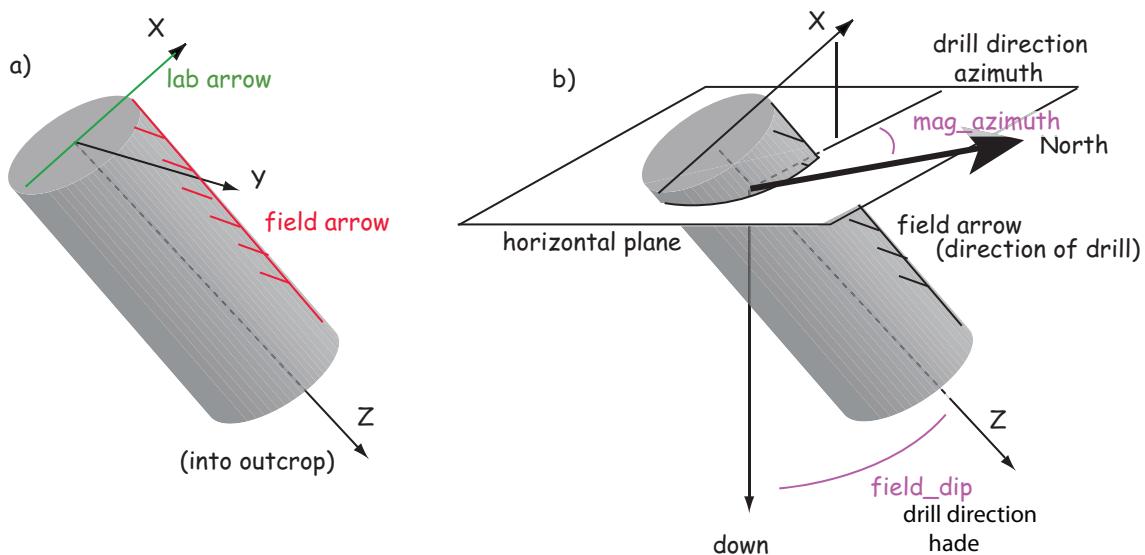
All images, for example outcrop photos are supplied as a separate zip file. *image_name* is the name of the picture you will import, *image_look* is the “look direction” and *image_photographer* is the person who took the picture. This information will be put in a file named *er_images.txt* and will ultimately be read into the *er_image* table in the console where additional information must be entered (keywords, etc.).

Often, paleomagnetists note when a sample orientation is suspect in the field. To indicate that a particular sample may have an uncertainty in its orientation that is greater than about 5° , enter SO-GT5 in the *method_codes* column and any other special codes pertaining to a particular sample from the *method codes* table. Other general method codes can be entered later. Note that unlike date and *sample_class*, the method codes entered in *orient.txt* pertain only to the sample on the same line.

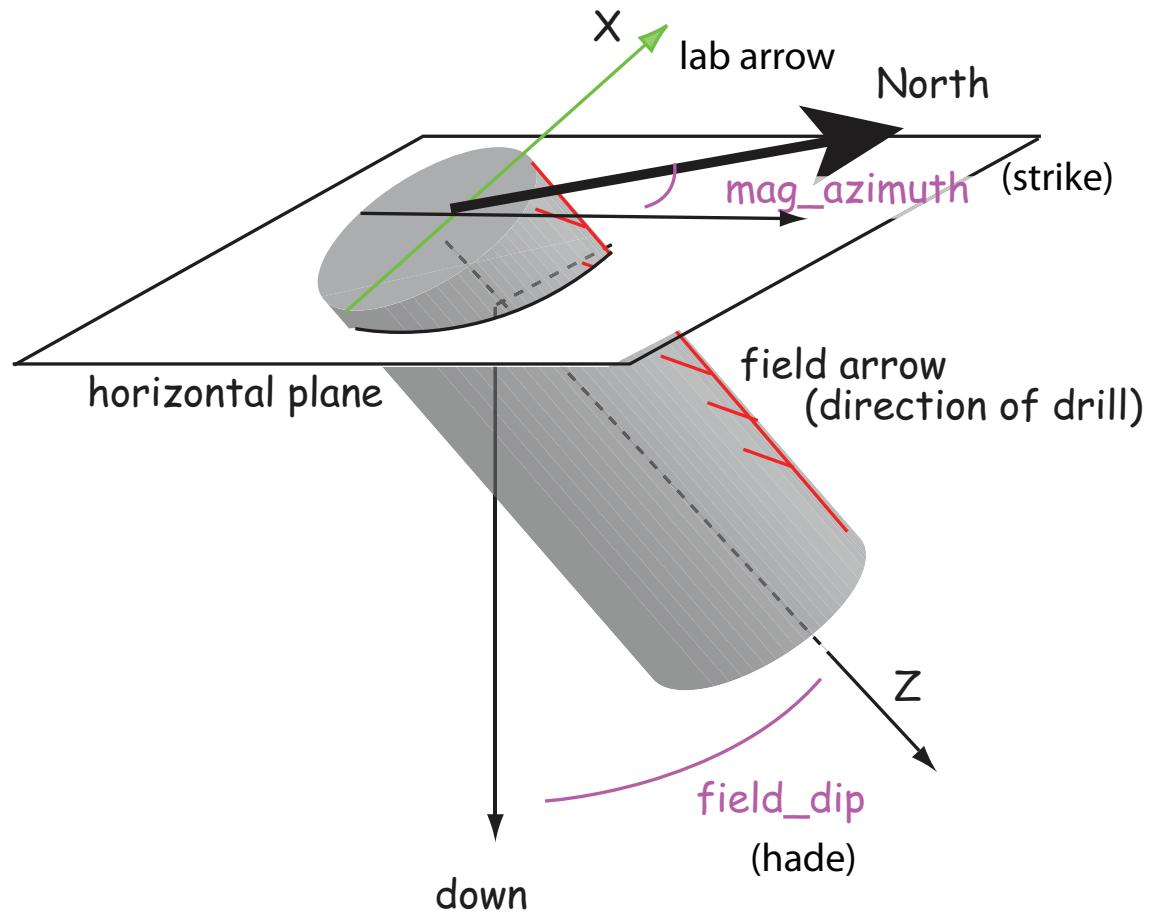
Samples are oriented in the field with a “field arrow” and measured in the laboratory with a “lab arrow”. The lab arrow is the positive X direction of the right handed coordinate system of the specimen measurements. The lab and field arrows may not be the same. In the MagIC database, we require the orientation (azimuth and plunge) of the X direction of the measurements (lab arrow). Here are some popular conventions that convert the field arrow azimuth (*mag_azimuth* in the *orient.txt* file) and dip (*field_dip* in *orient.txt*)

to the azimuth and plunge of the laboratory arrow (sample_azimuth and sample_dip in er_samples.txt). The two angles, mag_azimuth and field_dip are explained below.

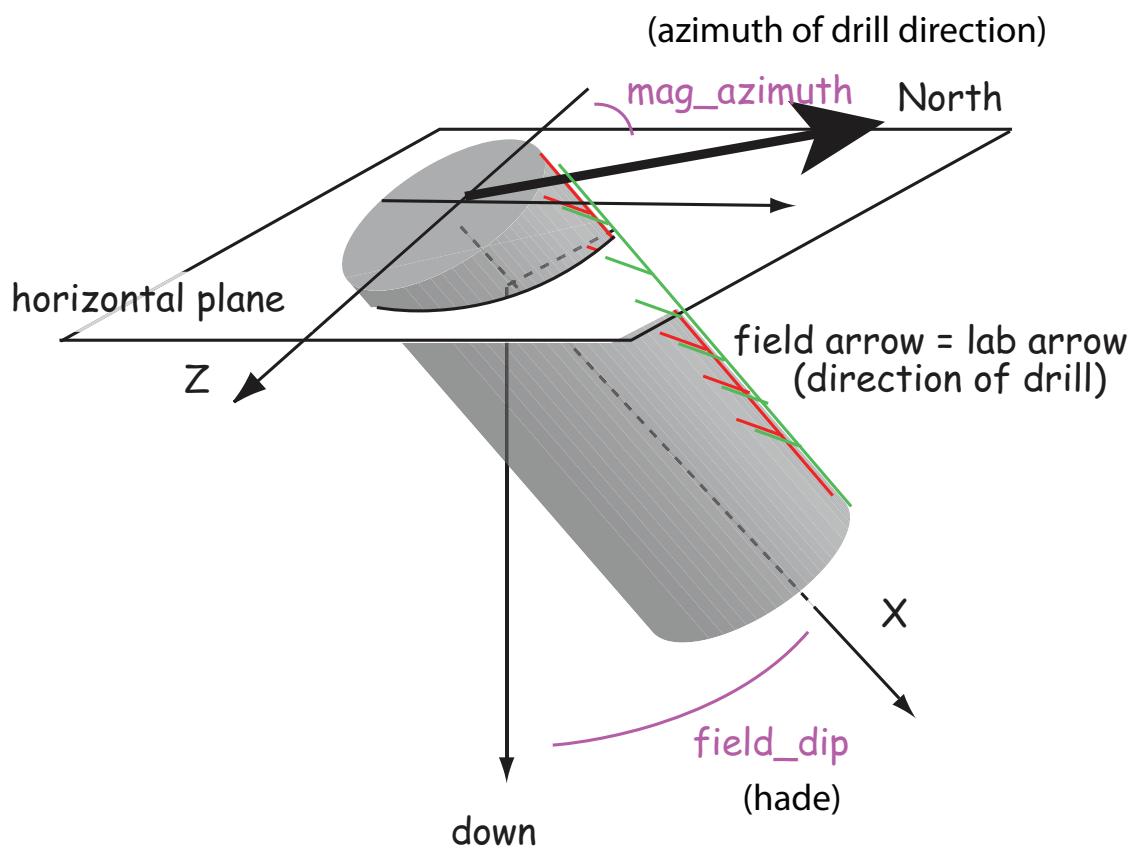
[1] Standard Pomeroy convention of azimuth and hade (degrees from vertical down) of the drill direction (field arrow). sample_azimuth = mag_azimuth; sample_dip = -field_dip.



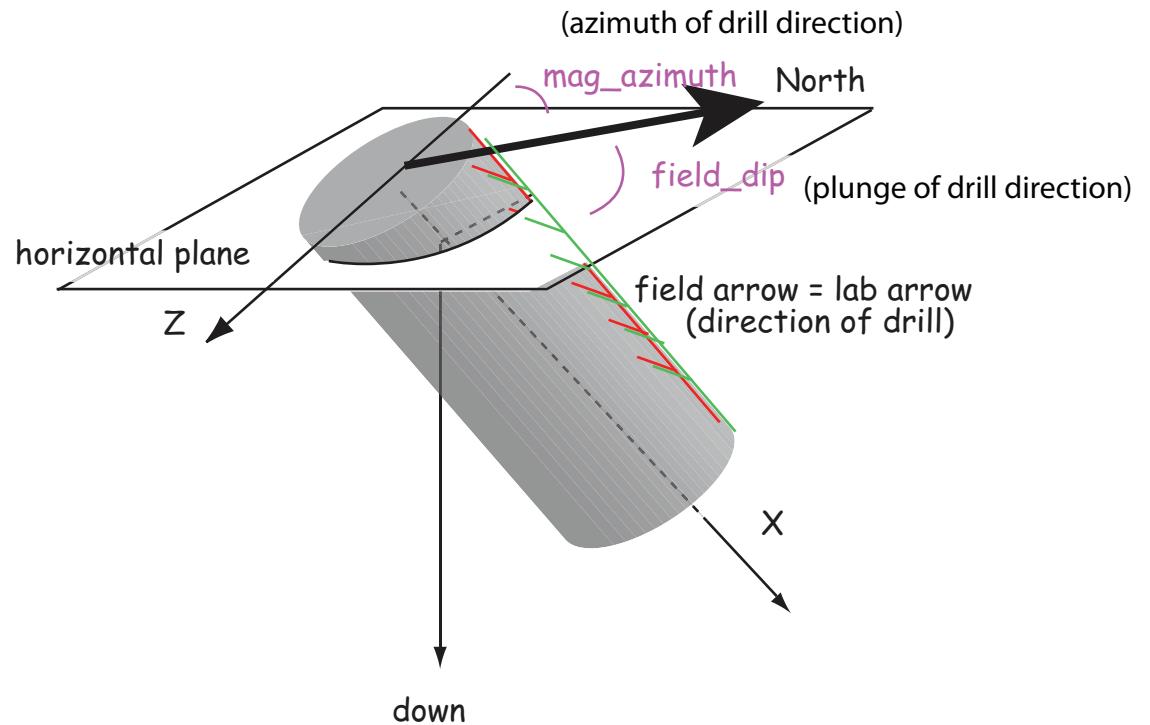
[2] Field arrow is the strike of the plane orthogonal to the drill direction, Field dip is the hade of the drill direction. Lab arrow azimuth = mag_azimuth-90°; Lab arrow dip = -field_dip



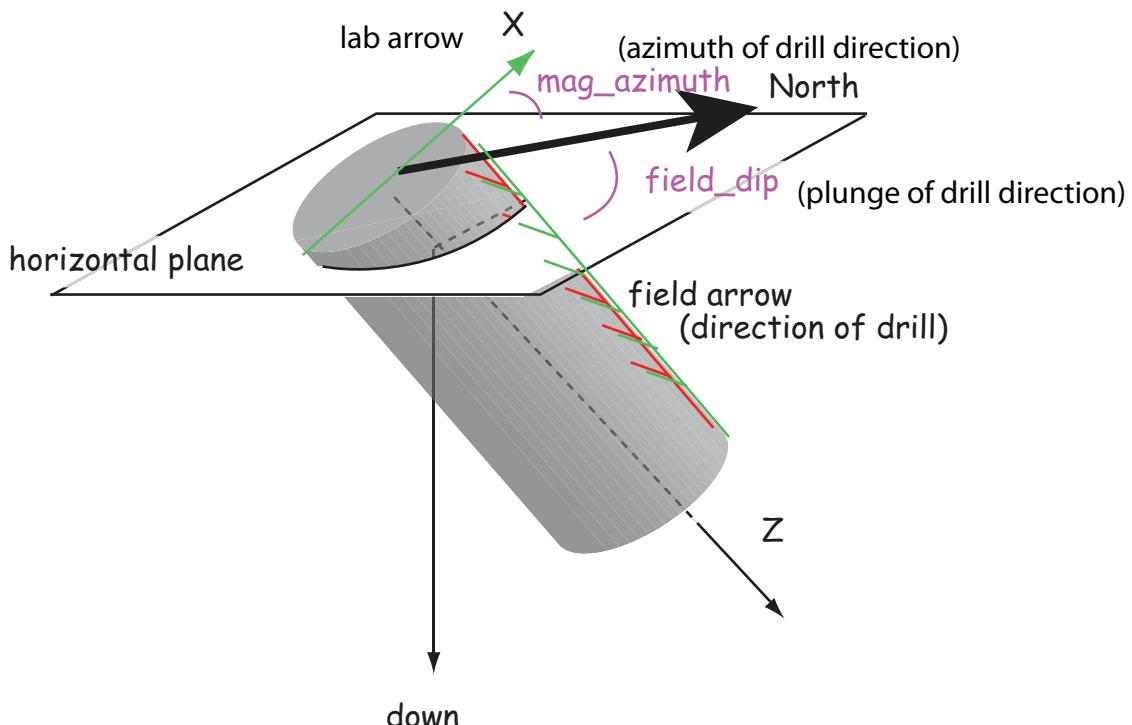
[3] Lab arrow is the same as the drill direction; hade was measured in the field. Lab arrow azimuth = mag_azimuth; Lab arrow dip = 90° -field_dip.



[4] Lab arrow orientation same as mag_azimuth and field_dip.



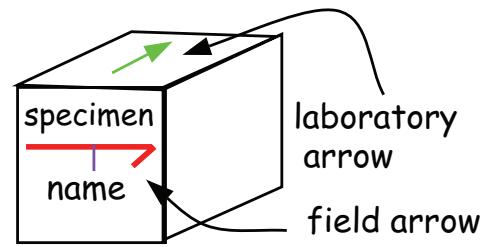
[5] Lab arrow azimuth is mag_azimuth and lab arrow dip is the field_dip-90°



[6] Lab arrow azimuth is $\text{mag_azimuth} - 90^\circ$, Lab arrow dip is $90^\circ - \text{field_dip}$, i.e., the field arrow was strike and dip of orthogonal face:

sample in the field

=> specimen in the lab



$\text{mag_azimuth} = \text{strike}$
 $\text{field_dip} = \text{dip}$

Structural correction conventions:

Because of the ambiguity of strike and dip, the MagIC database uses the dip direction and dip where dip is positive from $0 \rightarrow 180$. Dips > 90 are

overturned beds.

Supported sample naming schemes:

- [1] XXXXY: where XXXX is an arbitrary length site designation and Y is the single character sample designation. e.g., TG001a is the first sample from site TG001. [default]
- [2] XXXX-YY: YY sample from site XXXX (XXX, YY of arbitrary length)
- [3] XXXX.YY: YY sample from site XXXX (XXX, YY of arbitrary length)
- [4-Z] XXXX[YYY]: YYY is sample designation with Z characters from s
- [5] site name = sample name
- [6] site name entered in site_name column in the orient.txt format in
- [7-Z] [XXX]YYY: XXX is site designation with Z characters from samp

When you are finished with editing the *orient.txt* file, return to step 2 on the GUI front panel.

Data files downloaded from the IODP (LIMS) database

There are two types of files that help in plotting IODP paleomagnetic data sets: the core summaries with depth to core top information and the sample information that contains lists of samples taken. Visiting the IODP science query website at <http://web.iodp.tamu.edu/WTR/html/sci-data.html> allows you to select 'SRM - Remanence of magnetization' under the Analysis scroll down menu. By picking the expedition, site, hole, etc. you can download a .csv format (comma separated values) for the expedition data. (Be aware that this is the rawest form of the data, including disturbed intervals, bad measurements, core ends, etc. and may not be exactly what ended up getting published!). First click on the "Show Report" button, then, "Expand Table", then "Get File":

Web Tabular Report
IODP-USIO Laboratory Information Management System (LIMS)
 Version 3.0.0.9

(Optimized for Mozilla Firefox.)

[Home](#) [Summaries](#) [Samples](#) [Science-data](#)

Logged in as: guest | [Log in](#)

Science Data Search

*Analysis * QAQC QAQC & Report

EXPEDITION/SAMPLE		TEST/RESULT	
Expedition/Project	<input type="text" value="318"/> <input type="button" value="▼"/>	Alt. Depth Scale	<input type="text" value="SRM"/> <input type="button" value="▼"/>
Site	<input type="text" value="U1359"/> <input type="button" value="▼"/>	Core Type	<input type="text" value="Instrument"/> <input type="button" value="▼"/>
Hole	<input type="text" value="B"/> <input type="button" value="▼"/>	Section Half	<input type="text" value="W"/> <input type="button" value="▼"/>
Core	<input type="text" value=""/> <input type="button" value="▼"/>	OR	
Section	<input type="text" value=""/> <input type="button" value="▼"/>	Splice	<input type="text" value=""/> <input type="button" value="▼"/>

Text Id:

[Click here to download the results as a file.](#)

Query Results
 Total Count : 119

Label Id	Exp	Site	Hole	Core	Core Type	Section	Section Half	Interval Top (cm) on SECT	Interval Bot (cm) on SECT	CSF-A Top (m)	CSF-
318-U1359B- 21H-3-W 85/87-PMAG	318	U1359	B	21	H	3	W	85.00	87.00	192.05	192.0
318-U1359B- 21H-3-W 85/87-PMAG	318	U1359	B	21	H	3	W	85.00	87.00	192.05	192.0

This can take a very long time, so get yourself a cup of tea.

You can also (while you're at it) click on the 'Summaries' tab and download the coring summaries:

Web Tabular Report
IODP-USIO Laboratory Information Management System (LIMS)
Version 3.0.0.9

(Optimized for Mozilla Firefox.)

Home	Summaries	Samples	Science-data
Logged in as: guest Log in			
Summary Reports Select a report to get: <input style="border: 1px solid black; padding: 2px; width: 150px; height: 20px; margin-bottom: 5px;" type="button" value="Core Summary"/> <input style="border: 1px solid black; padding: 2px; width: 150px; height: 20px; margin-bottom: 5px;" type="button" value="Splice Summary"/> Select a date range for the report: (optional) Start: <input style="width: 100px; height: 20px; border: 1px solid black; margin-right: 10px;" type="text"/> (mm/dd/yyyy) Finish: <input style="width: 100px; height: 20px; border: 1px solid black; margin-left: 10px;" type="text"/> (mm/dd/yyyy) Select other filters for the report: (optional) Expedition: <input style="border: 1px solid black; padding: 2px; width: 100px; height: 20px; margin-bottom: 5px;" type="button" value="318"/> <input style="border: 1px solid black; padding: 2px; width: 20px; height: 20px; margin-bottom: 5px;" type="button" value="▼"/> Site: <input style="border: 1px solid black; padding: 2px; width: 100px; height: 20px; margin-bottom: 5px;" type="button" value="U1359"/> <input style="border: 1px solid black; padding: 2px; width: 20px; height: 20px; margin-bottom: 5px;" type="button" value="▼"/> Hole: <input style="border: 1px solid black; padding: 2px; width: 100px; height: 20px; margin-bottom: 5px;" type="button" value="B"/> <input style="border: 1px solid black; padding: 2px; width: 20px; height: 20px; margin-bottom: 5px;" type="button" value="▼"/> Core: <input style="border: 1px solid black; padding: 2px; width: 100px; height: 20px; margin-bottom: 5px;" type="button" value=" "/> <input style="border: 1px solid black; padding: 2px; width: 20px; height: 20px; margin-bottom: 5px;" type="button" value="▼"/> Section: <input style="border: 1px solid black; padding: 2px; width: 100px; height: 20px; margin-bottom: 5px;" type="button" value=" "/> <input style="border: 1px solid black; padding: 2px; width: 20px; height: 20px; margin-bottom: 5px;" type="button" value="▼"/> OR Splice: <input style="border: 1px solid black; padding: 2px; width: 100px; height: 20px; margin-bottom: 5px;" type="button" value=" "/> <input style="border: 1px solid black; padding: 2px; width: 20px; height: 20px; margin-bottom: 5px;" type="button" value="▼"/> <input style="border: 1px solid black; padding: 2px; width: 100px; height: 20px; margin-right: 20px;" type="button" value="Show Report"/> <input style="border: 1px solid black; padding: 2px; width: 100px; height: 20px; margin-right: 20px;" type="button" value="Download File"/> <input style="border: 1px solid black; padding: 2px; width: 100px; height: 20px; margin-right: 20px;" type="button" value="Reset"/> <input style="border: 1px solid black; padding: 2px; width: 100px; height: 20px; margin-right: 20px;" type="button" value="Expand Table"/> <input style="border: 1px solid black; padding: 2px; width: 100px; height: 20px;" type="button" value="Print Table"/>			

Core Summary Report for Expedition 318, Site U1359, Hole B Generated On 09/07/2012 19:40

Label ID	Expedition	Site	Hole	Core #	Core Type	Core Top (m)	Advanced (m)	Cored bottom (m)	Recovered Length (m)
318-U1359B-1H	318	U1359	B	1	H	0.0	7.7	7.7	7.74
318-U1359B-2H	318	U1359	B	2	H	7.7	9.5	17.2	9.15

Place both of the downloaded files in your *MyFiles* directory.

2.8.2 Supported Rock Magnetometer files

The MagIC database is designed to accept data from a wide variety of paleo-magnetic and rock magnetic experiments. Because of this the magic_measurements table is complicated. Each measurement only makes sense in the context of what happened to the specimen before measurement and under what conditions the measurement was made (temperature, frequency, applied field, specimen orientation, etc). Also, there are many different kinds of instru-

ments in common use, including rock magnetometers, susceptibility meters, Curie balances, vibrating sample and alternating gradient force magnetometers, and so on. We have made an effort to write translation programs for the most popular instrument and file formats and continue to add new supported formats as the opportunity arises. Here we describe the various supported data types and tell you how to prepare your files for importing. In general, all files for importing should be placed in the MyFiles directory or in subdirectories therein as needed. If you don't see your data type in this list, please send an example file and a request to: ltauxe@ucsd.edu and we'll get it in there for you.

The supported file formats are:

Rock Magnetometer Files:

- The CalTech format used by labs in the RAPID consortium
- Hebrew University, Jerusalem format
- Scripps Institution of Oceanography format
- Lamont Doherty Earth Observatory format
- IODP rock magnetometer (SRM) data downloaded from the LIMS database
- PMD (ascii) format
- ThellierTool format

Anisotropy of Magnetic Susceptibility files:

- The 6 tensor element format (.s)
- LabView program of Gee et al. 2008
- 15 measurement convention of Tauxe 1998
- SUFAR 4.0 ascii output for Kappabridge

Hysteresis file formats

Pmag GUI will import hysteresis data from room temperature Micromag alternating gradient magnetometers (AGM) in several different ways. You can import either hysteresis loops or backfield curves, or you can import whole directories of the same. In the latter case, the file endings must be

either .agm (.AGM) or .irm (.IRM) and the first part of the file must be the specimen name. See the documentation for AGM_magic.py for examples.

Now you've collected together all the files you need, we can start importing them into *MagIC* directory with **Step 1 in Pmag GUI**.

Chapter 3

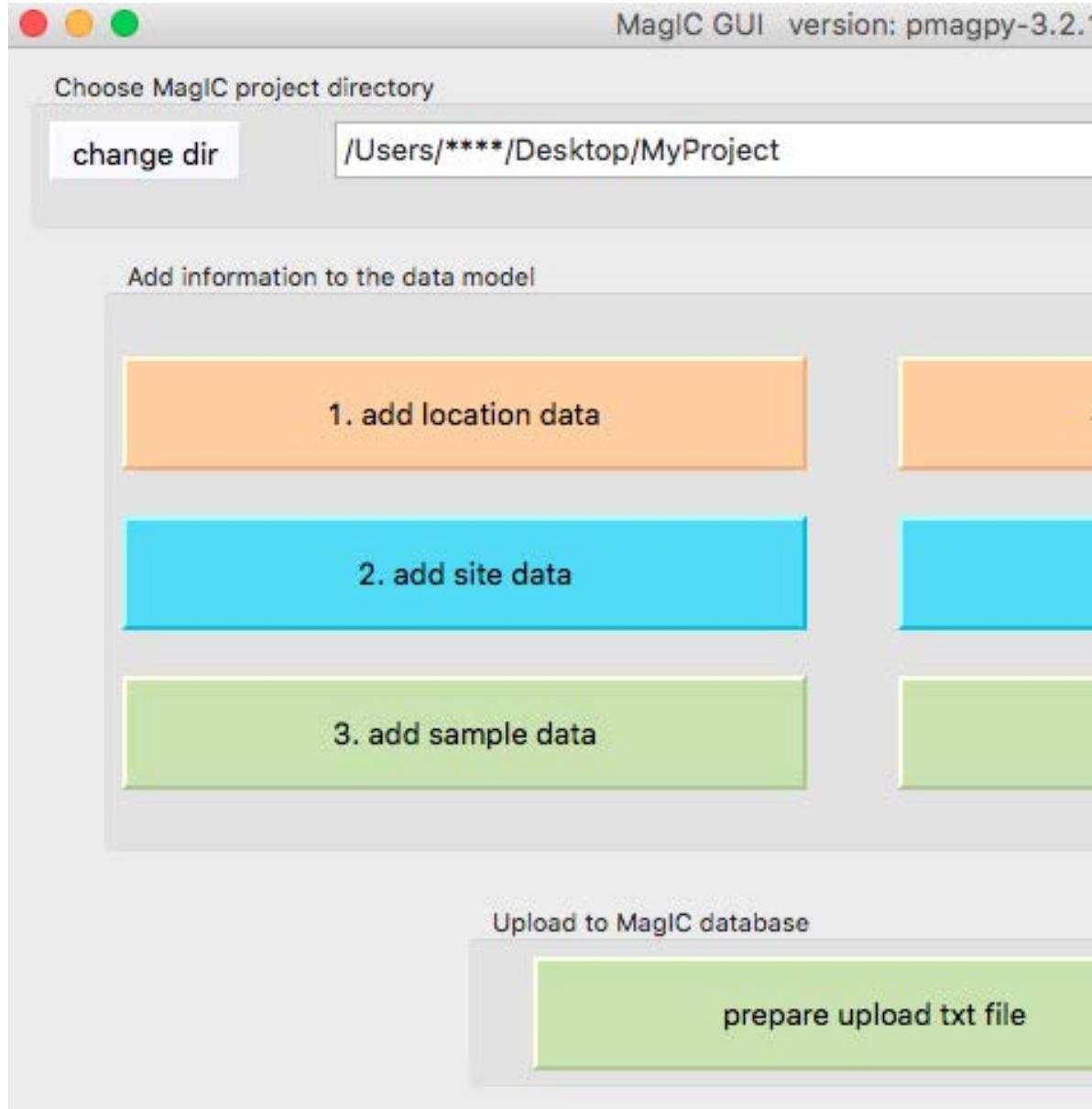
MagIC GUI Tutorial

MagIC GUI is a Graphical User Interface written by Lori Jonestrask. It is meant for efficiently compiling a contribution for uploading to the MagIC database. MagIC GUI is specifically designed for making a contribution without measurement data; if you ARE including measurement data, we recommend that you use Pmag GUI instead. MagIC GUI allows you to add data at the location, site, sample, and specimen levels. You can also add results and ages. The program uses an Excel-like grid interface for entering and editing data. Useful features include: pop-up menus with controlled vocabularies, multi-cell pasting from external spreadsheets, and built-in validations for MagIC database requirements.

3.1 Starting with MagIC GUI

Start up MagIC GUI. You'll do this by clicking on the icon (if you downloaded the standalone version) or entering ‘magic_gui.py’ on your command line (if you downloaded the full PmagPy installation).

When you first start **magic-gui.py**, you will change directories into a ‘Project Directory’. For each study, create a directory with a name that relates to that study. Here we will call it *MyProject*. This is where you will collect and process all the rock and paleomagnetic data for a given study, usually a publication. The project directory name should have NO SPACES and be placed on the hard drive in a place that has NO spaces in the path. Under certain Windows versions, this means you should not use your home directory, but create a directory called for example: D:\MyPmagProjects and put *MyProject* there.

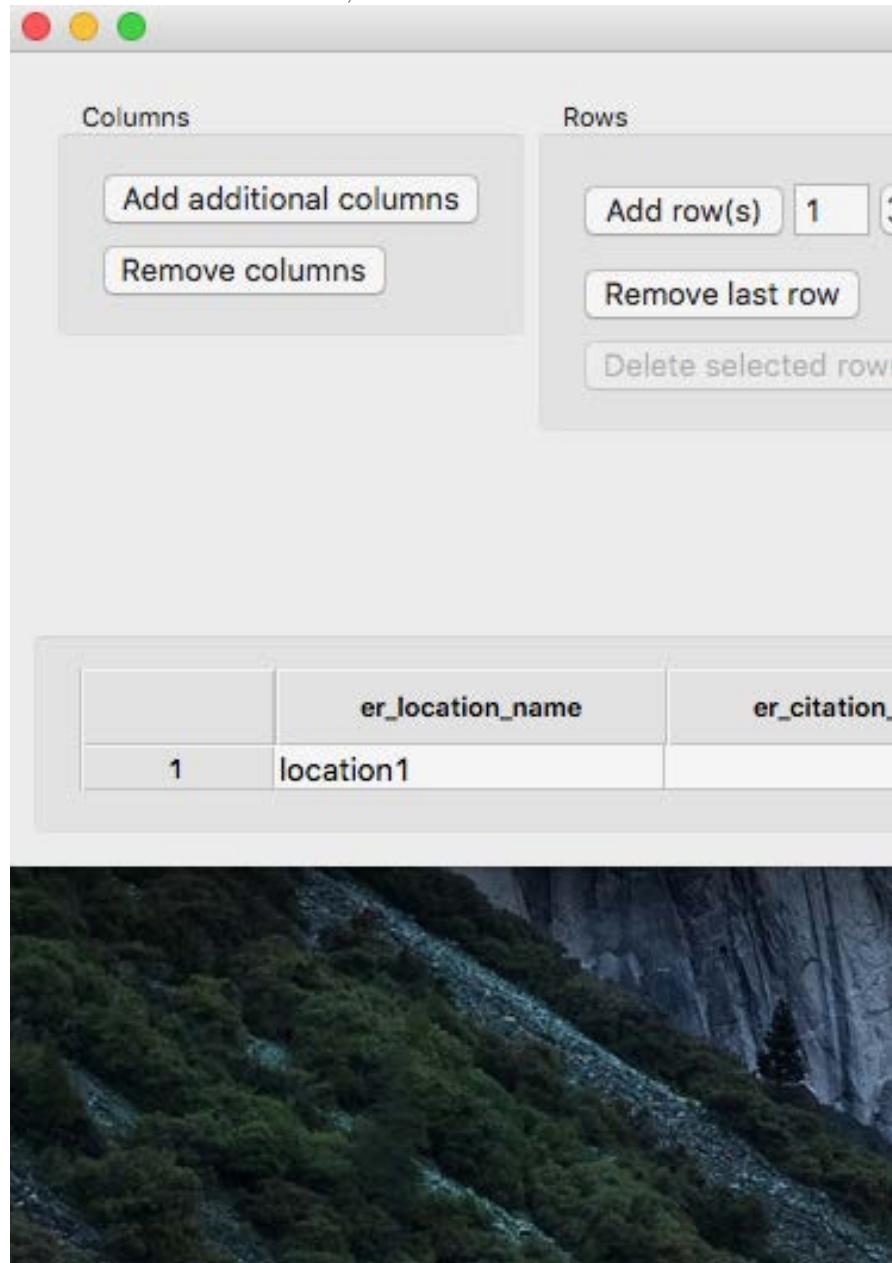


3.2 MagIC GUI example dataset

Now we'll walk through a simple data input process, with fake data.

- Start by clicking on '1. add location data'. Enter location data as seen

below. Notice use of the context menu: in most instances, these will

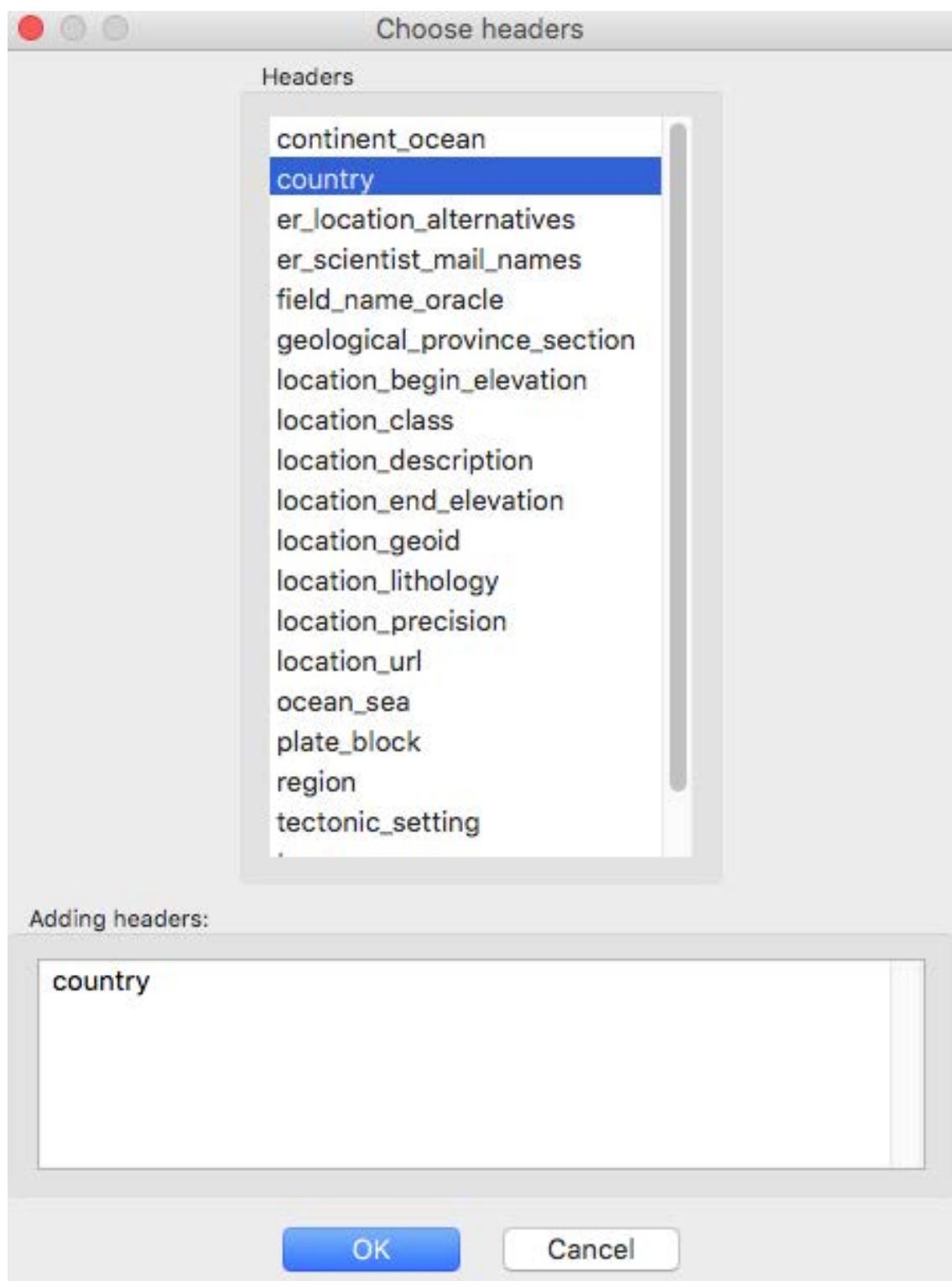


provide controlled vocabularies.

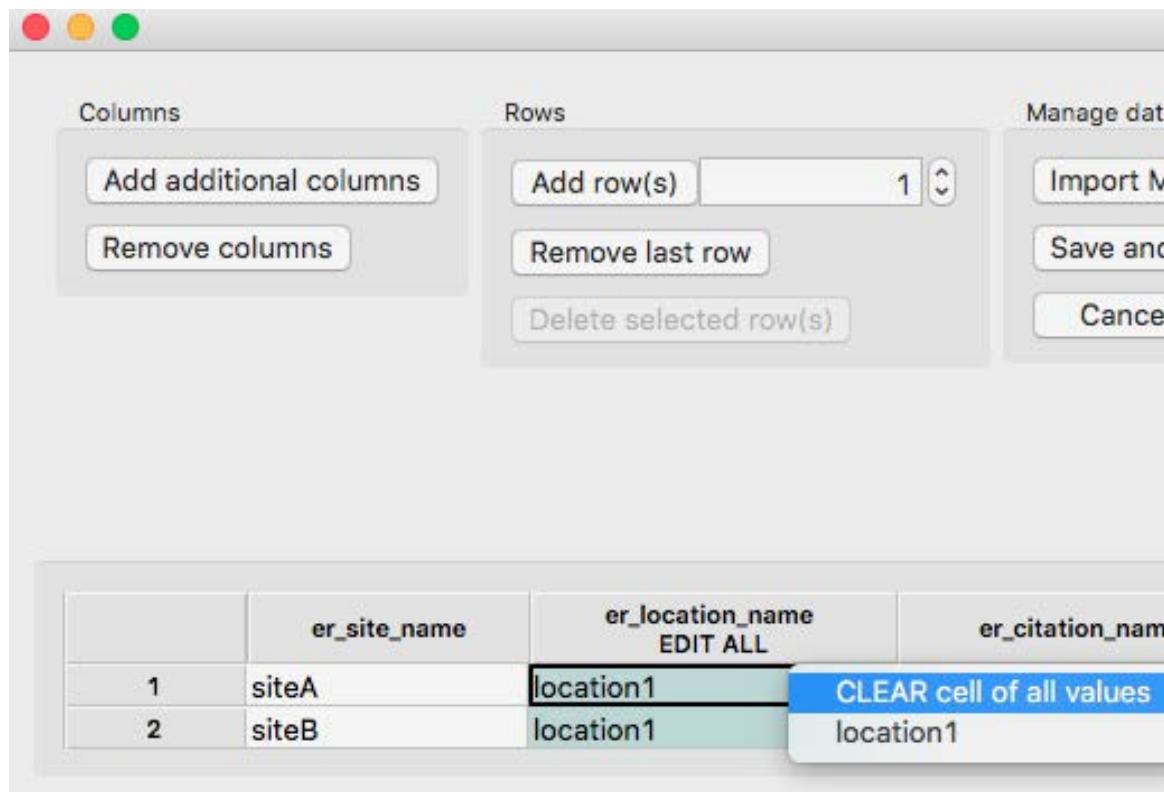
- You'll notice that some information is not filled in. First, if you have no outside citations, you can leave 'er_citation_names' blank and it will be automatically filled in with 'This study' after you save this data.

Second, if you will be providing latitude/longitude for sites, then you don't need to provide it at the location level. The program will extract start and end latitude and longitude from your site data and apply it to each location.

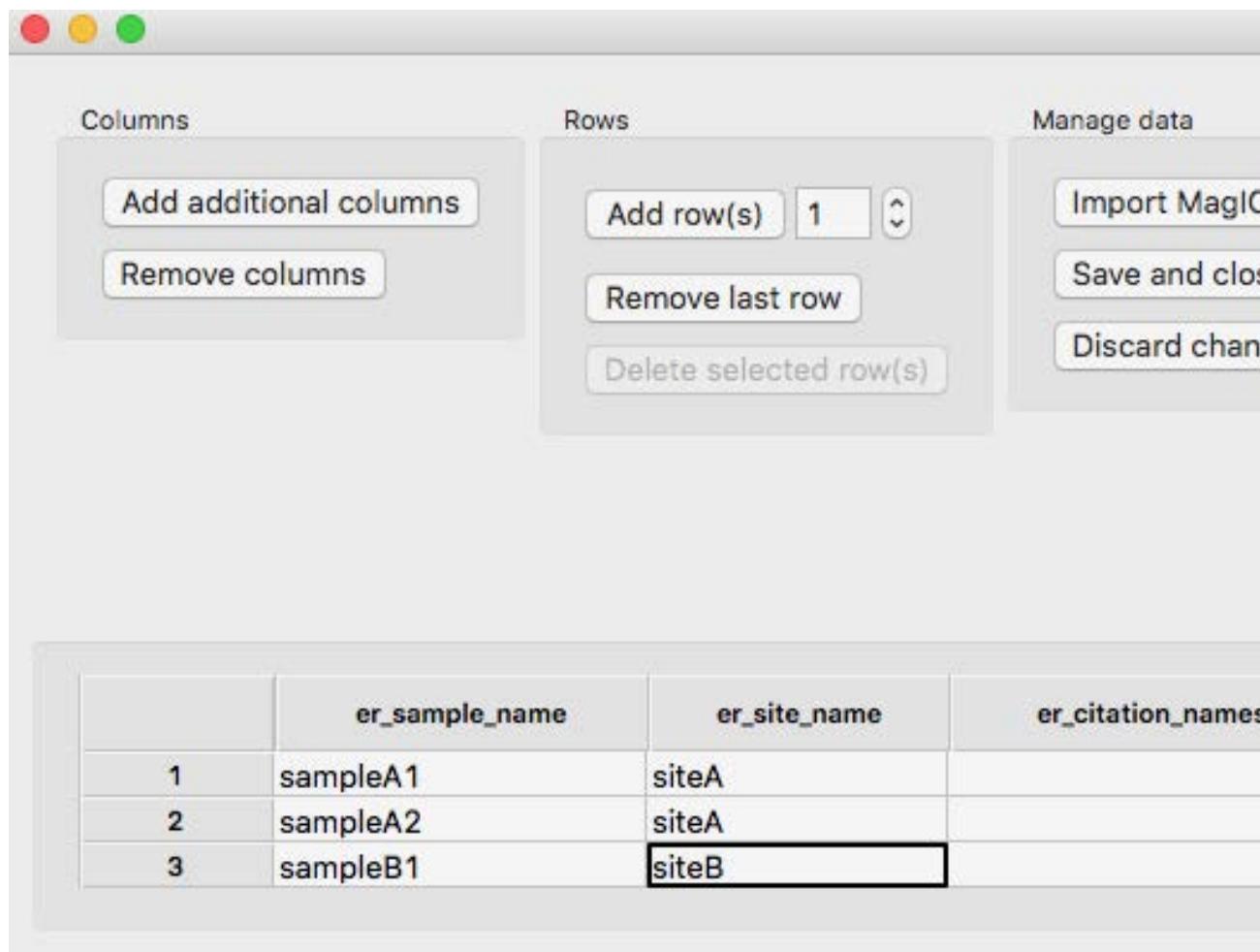
- If you want to provide more than the default required information, you may want to add more columns to your grid. In our case, we'll add in 'Country'. To do this, just click the button 'Add additional columns'. Choose whatever headers you want to add and select 'Ok'.



- Now you'll have a new column with a new controlled vocabulary. Find and select 'U.S.A.'. When you're done entering location data, click 'Save and close grid'.
- Next, we'll add in sites, so start by opening the site grid. We will have two sites in this dataset, so click the 'Add row(s)' button once. Then, fill in the grid. For some of the values, both sites will have the same value. To provide this data more efficiently, click on the column label to edit all values in that column. If that column has a menu, you can then click anywhere in that column and make a selection for every cell in the column. If that column has a menu, you can then click anywhere in that column and make a selection for every cell in the column. Once you're done editing the column, click the header again to exit the multiple-cell-edit mode.
- For controlled vocabulary columns, like 'site_type', it is possible that you might not be able to find an appropriate value, or you might not know the appropriate value. In that case, most controlled vocabularies provide a 'Not Specified' option, which we will use here.



- Once you're done adding sites, save and close the site grid, then open the sample grid. Enter data as you see below:



The screenshot shows the MAGIC GUI interface for managing datasets. At the top, there are three colored buttons (red, yellow, green) and tabs for 'Columns' and 'Rows'. On the right, there's a 'Manage data' panel with buttons for 'Import MagIC...', 'Save and close', and 'Discard changes'. The main area displays a table with three rows. The first two rows have 'er_sample_name' values 'sampleA1' and 'sampleA2' respectively, and 'er_site_name' values 'siteA'. The third row has 'er_sample_name' value 'sampleB1' and 'er_site_name' value 'siteB', which is highlighted with a black border.

	er_sample_name	er_site_name	er_citation_names
1	sampleA1	siteA	
2	sampleA2	siteA	
3	sampleB1	siteB	

All other required data will fill in automatically. If you don't provide latitude and longitude data for a sample, it will propagate down from the site after you save and close the grid.

- For samples, we will add an additional statistic. Click 'Add additional columns' and select 'sample_int_sigma' from the 'Headers for interpretation data' column. Select 'ok' and have a look at your new grid. You'll notice that the column you selected has been added, as well as two additional columns: 'magic_instrument_codes' and 'magic_method_codes++'. These two columns are required if you are including any interpretation

data at the sample level. Fill in the added columns. You'll notice that ‘magic.method.codes++’ has a drop-down menu. If you aren't familiar with the MagIC codes system, click ‘Show method codes’ which provides brief explanations for each possible code.

The screenshot shows a window titled "MAGIC GUI EXAMPLE DATASET". At the top, there are three colored buttons (red, yellow, green) and a title bar. Below the title bar is a toolbar with several buttons: "Columns", "Rows", "Manage data", "Import MagIC-format file", "Save and close grid", and "Cancel".

The "Columns" section contains two buttons: "Add additional columns" and "Remove columns".

The "Rows" section contains three buttons: "Add row(s)" (with a dropdown menu showing "1"), "Remove last row", and "Delete selected row(s)".

The "Manage data" section contains three buttons: "Import MagIC-format file", "Save and close grid", and "Cancel".

To the right of the toolbar is a vertical list of processing steps:

- Anisotropy Estimation
- Intensity Estimation
- Sample Preparation

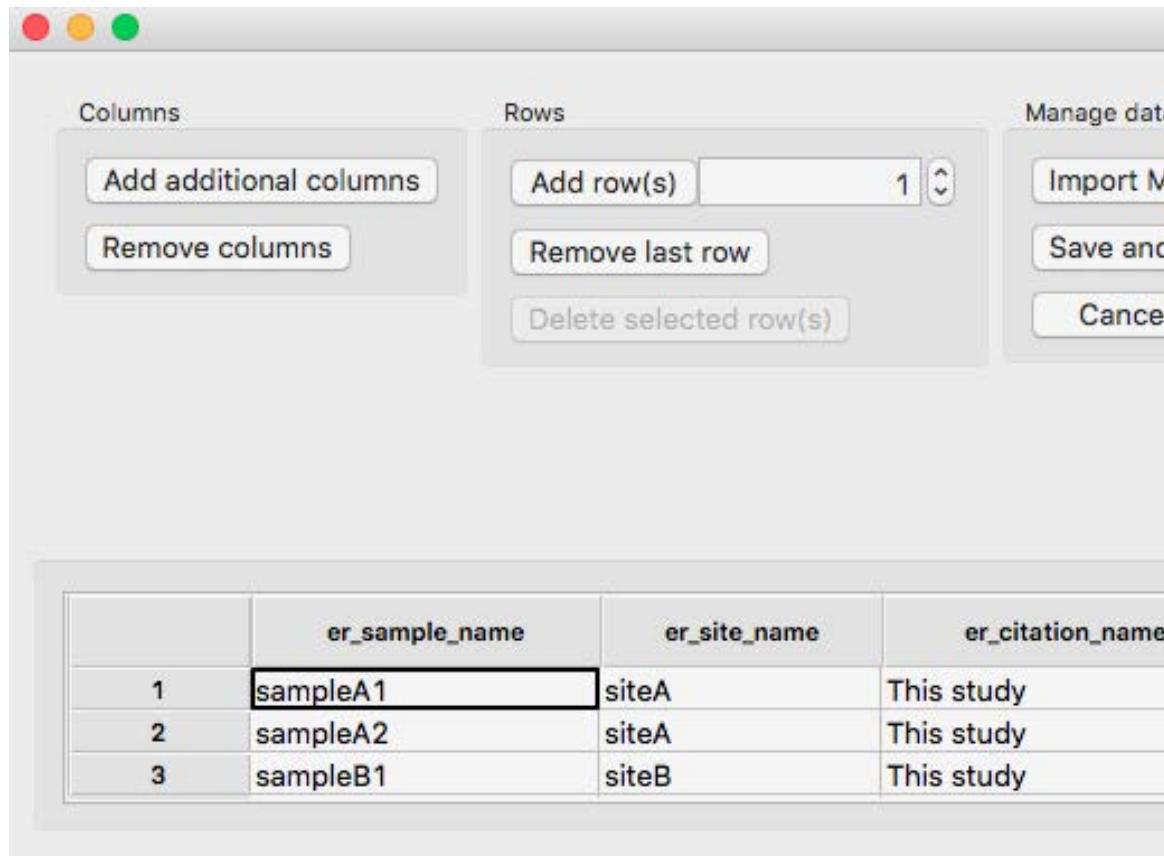
Below these are several options starting with "LP-DIR":

- LP-DIR : Directional
- LP-DIR-AF : Directional
- LP-DIR-AF-D : Directional
- LP-DIR-AF-G : Directional
- LP-DIR-M : Directional
- LP-DIR-T : Directional
- LP-DM-NRM : Demagnetization
- LP-DM-SIRM : Demagnetization
- LP-FC : Field cooled

At the bottom of the window is a table with four columns:

	er_sample_name	er_site_name	er_citation_names
1	sampleA1	siteA	
2	sampleA2	siteA	
3	sampleB2	siteB	

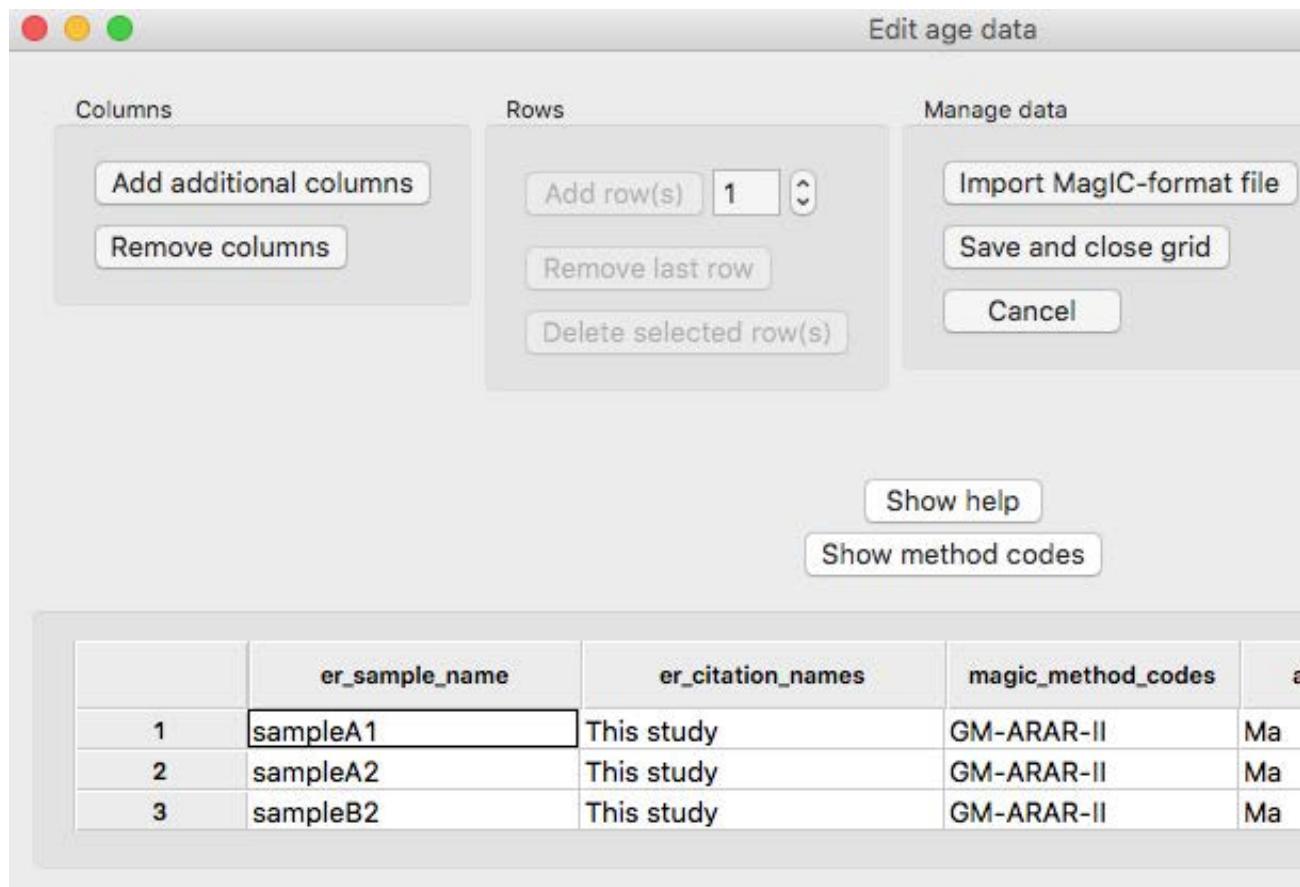
- Save and close the sample grid, then re-open it to see how the data have propagated (re-opening the grid isn't necessary for the program, this is just for you to see what MagIC GUI does automatically).



The screenshot shows a Mac OS X style window titled "Manage data". On the left, there are two sections: "Columns" containing "Add additional columns" and "Remove columns" buttons; and "Rows" containing "Add row(s)" (with a dropdown set to 1), "Remove last row", and "Delete selected row(s)" buttons. Below these sections is a large table with four columns: "er_sample_name", "er_site_name", and "er_citation_name". The first column contains numerical IDs (1, 2, 3). The second column contains specimen names ("sampleA1", "sampleA2", "sampleB1"). The third column contains site names ("siteA", "siteA", "siteB"). The fourth column contains citation names ("This study", "This study", "This study"). The row for specimen 1 is currently selected, as indicated by a black border around its entire row.

	er_sample_name	er_site_name	er_citation_name
1	sampleA1	siteA	This study
2	sampleA2	siteA	This study
3	sampleB1	siteB	This study

- In this example, we won't add data at the specimen level, so we will be skipping step 4. Adding specimens works just the same as adding samples.
- Now open the age grid. You can assign ages at any level, at multiple levels, or at no level. For this study, we will add ages at the sample level. Choose sample as the age level. Next, you'll need to add in the 'age' column. Fill in the grid as below:

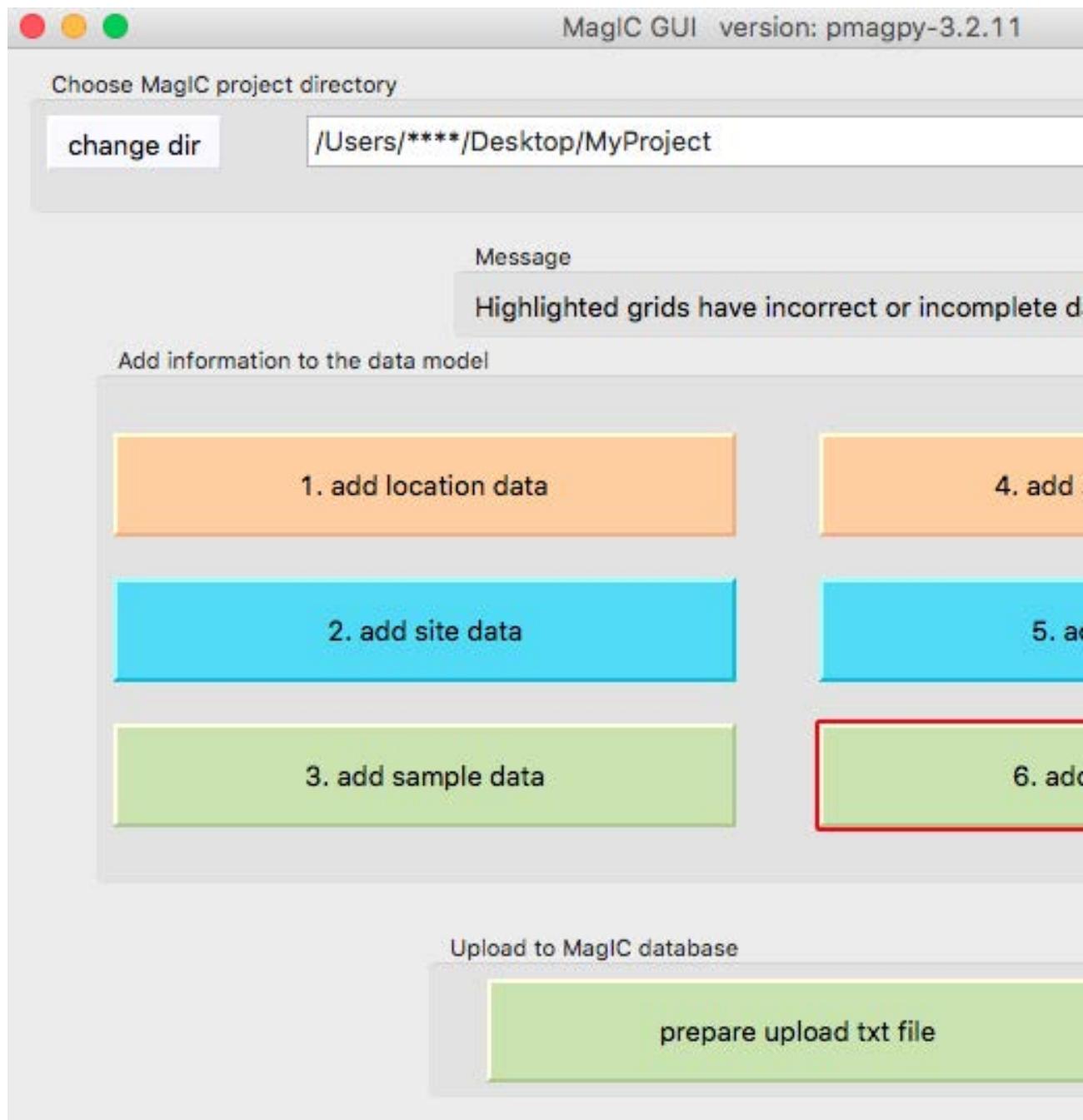


- You'll notice that you can't add or remove rows in this grid. If you want to add an additional sample, you would need to go back to the sample grid to do so.
- The last data step is to put in result information. You'll need to open the result grid and, for this example, add just one statistic: 'vadm'. Then, fill out the grid:

The screenshot shows a Mac OS X style dialog box titled "result grid". It has three main sections: "Columns" (with "Add additional columns" and "Remove columns" buttons), "Rows" (with "Add row(s)" set to 1, "Remove last row", and "Delete selected row(s)" buttons), and "Manage data" (with "Import MagIC-format t", "Save and close grid", and "Cancel" buttons). Below these sections is a table with the following data:

	pmag_result_name	er_citation_names	er_specimen_names
1	Average of all V [A] DMs	This study	
2	V[A]DM: siteA	This study	

- For each result, you will add one or more items that the result pertains to. In this example, one result is a site V[A]DM, and the other is an averaged V[A]DM from both sites. For now, leave `magic_method_codes` blank for the Averaged V[A]DM result: in a minute we'll see how MagIC GUI catches this error. Save and close the result grid.
- Next, you will create a MagIC format upload file. Click the final button on the main frame, ‘prepare upload txt file’. Depending on the size of your contribution, this can take a minute; with our small example, it should be fairly quick. After hitting upload, you will see an error message, and the main frame will direct you to the problem. Validations will check for missing required fields, invalid data, and missing ancestors (for instance, a specimen with no sample).



Open the result grid to fix the error. Click ‘Show help’ for more information about validations. In this case, it is a simple fix: add

method code ‘LP-PI’ to the average V[A]DM result.

	pmag_result_name	er_citation_names	er_specimen_names
1	Average of all V [A] DMs	This study	
2	V[A]DM: siteA	This study	

- Now that you’ve fixed your error, try ‘prepare upload txt file’ again. This time there should be no problems, and you are ready to upload your data!

Chapter 4

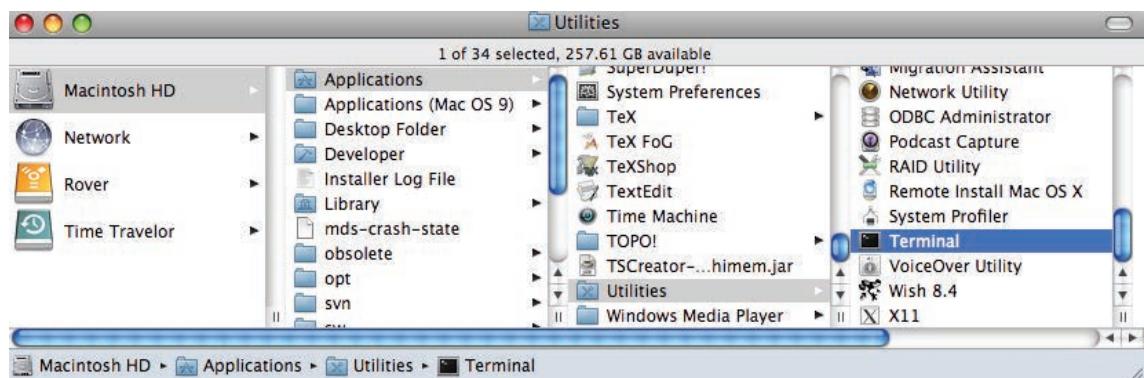
Survival computer skills

The ‘Py’ part of ‘PmagPy’ stands for Python, the language in which all the code is written. It is not essential, but it is helpful to understand a bit about computer operating systems and the Python language when using PmagPy because no one should be using programs as black boxes without understanding what they are doing. As all the programs are open source, you have the opportunity to look into them. If you understand a bit about how computers work yourself, you will be able to follow along what they are doing and even modify them to work better for you. So in this chapter you will find a brief introduction to the computer skills necessary for using the programs properly. We have tried very hard to make this tutorial operating system independent. All the examples should work equally well on Mac OS, Windows and Unix-type operating systems. For a more complete explanation of the marvelous world of UNIX, refer to the website at <http://www.tutorialspoint.com/unix/unix-quick-guide.htm>. For handy tricks in DOS, try this link: <http://www.c3scripts.com/tutorials/msdos>. For an introduction to programming in Python, see the Chapter on Python Programming. For now, we’re just interested in getting started with PmagPy.

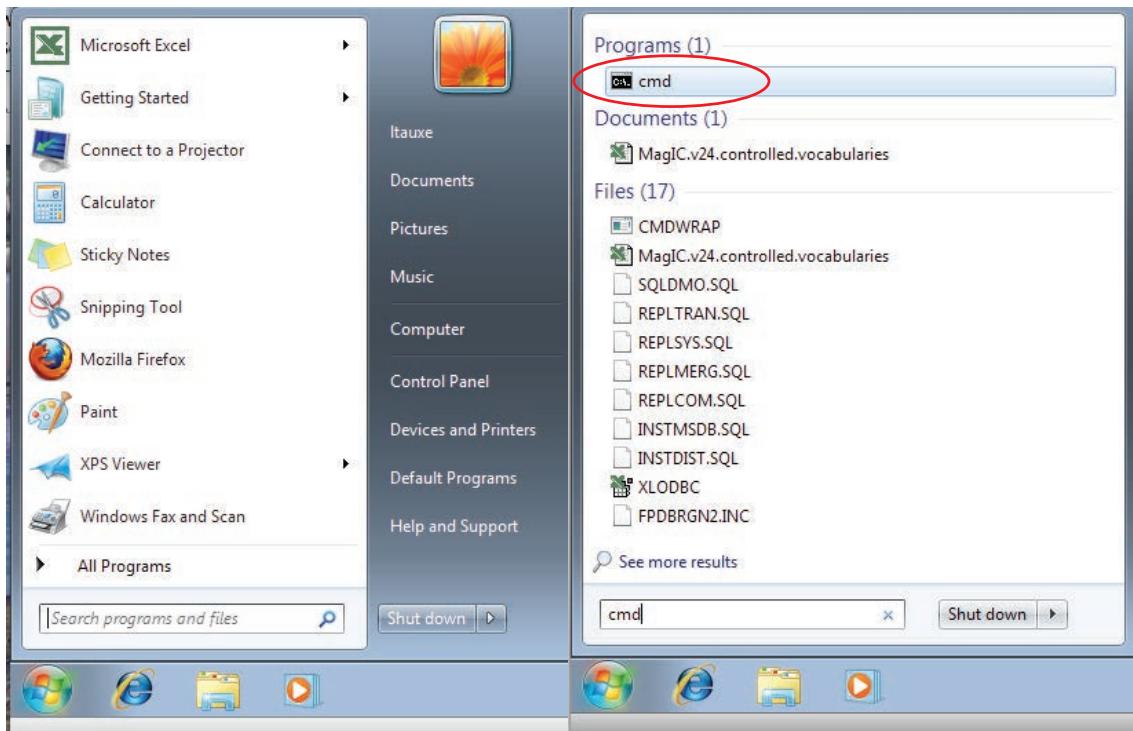
4.1 Finding your command line

If you are not using a Unix-like computer (*NIX), you may never have encountered a command line. While the Pmag GUI is an attempt to make life as easy for you by constructing commands for you, you still need to find the command line to start it up. Under the MacOS X operating system look for the Terminal application in the Utilities folder within the Applications folder. When it is launched, you will get a terminal window as shown below.

The Unix (and Mac OS) Bash shell has a \$ sign as a prompt. I (LT) use the antiquated ‘C-shell’ (don’t ask) with a % for a prompt and will use the % prompt in the examples here, but any of these command line prompts will work.



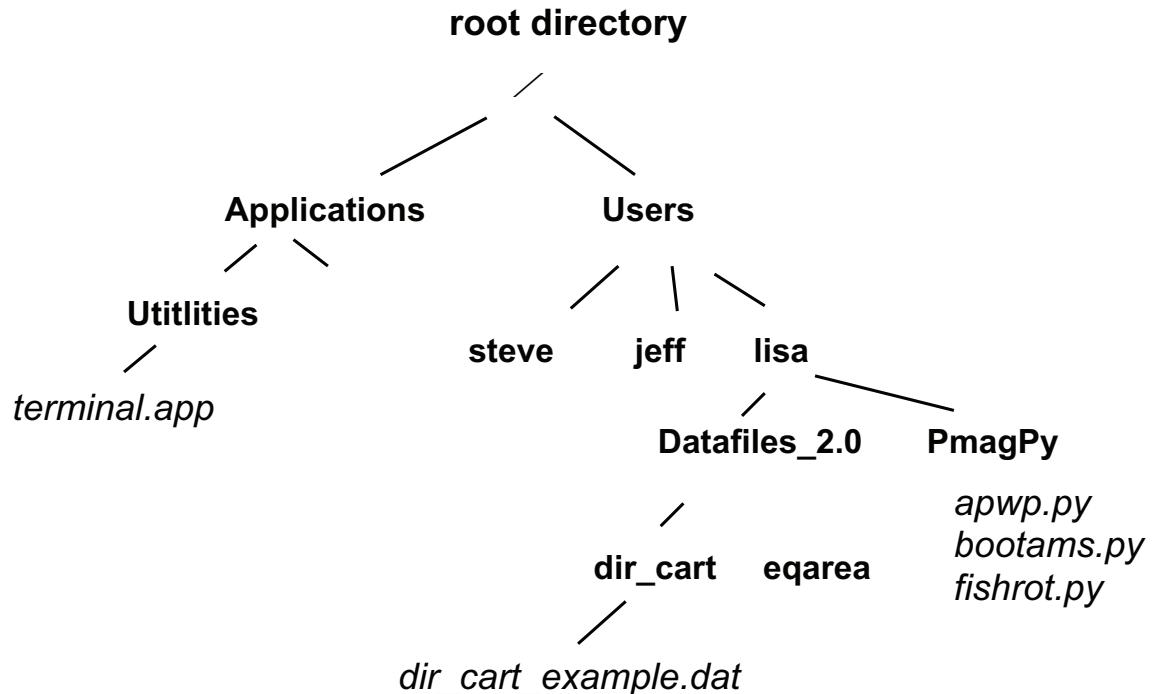
Under the Windows operating system, you can find your command line by searching for the “cmd” application. You’ll use this if you are using the full pip installation of PmagPy. If you are doing the standard PmagPy install, you will create a shortcut to the PmagPy command window on your desktop. Double clicking on that will give you a window in which you can type **PmagPy** commands. You will use the PmagPy prompt instead of the Windows command line from there on.



Note that the location of this program varies on different computers, so you may have to hunt around a little to find yours. Also, the actual “prompt” will vary for different machines.

4.2 File systems

When you open one of these terminal windows, you are in your “home” directory. Fundamental to all operating systems is the concept of directories and files. On windows-based operating systems (MacOS or Windows), directories are depicted as “folders” and moving about is accomplished by clicking on the different icons. In the world of terminal windows, the directories have names and are arranged in a hierarchical sequence with the top directory being the “root” directory, known as “/” (or C:\backslash\ in Windows) and the file system looks something like this:



Within the root directory, there are subdirectories (e.g. **Applications** and **Users** in bold face). In any directory, there can also be “files” (e.g. *dir_cart_example.dat* in italics). To refer to directories, the operating system relies on what is called a “ pathname”. Every object has an “absolute” pathname which is valid from anywhere on the computer. The absolute pathname in *NIX always begins from the root directory / and in DOS (the operating system working in the Windows command line window), it is C:\backslash’.

The absolute pathname to the home directory **lisa** in the figure is /**Users/lisa**. Similarly, the absolute pathname to the directory containing **PmagPy** scripts would be /**Users/lisa/PmagPy**. There is also a “relative” pathname, which is in reference to the current directory (the one you are ‘sitting’ in). If user “lisa” is sitting in her home directory, the relative pathname for the file *dir_cart_example.dat* in the directory **data_files** would be *data_files/dir_cart/dir_cart_example.dat*. When using relative pathnames, it is useful to remember that ./ refers to the current directory and ../ refers to the directory “above”. Also, lisa’s home directory would be ~lisa, or if you are logged in as lisa yourself, then it is just ~.

4.3 Moving around in the file system

Now that you have found your command line and are comfortable in your home directory, you can view the contents of your directory with the Unix command **ls** or the DOS command **dir**. You can make a new directory with the command

```
%mkdir NEW_DIRECTORY_NAME
```

This works in both Unix and DOS environments) and you can move into your new directory with the command

```
% cd NEW_DIRECTORY_NAME
```

To move back up into the home directory, just type **cd ..** remembering that .. refers to the directory above. Also, **cd** by itself will transport you home from where ever you are (there's no place like home....). You can also change to any arbitrary directory by specifying the full path of the destination directory.

4.4 Redirecting input and output

Programs that operate at the command line level print output to the screen and read input from the keyboard. This is known as “standard input and output” or “standard I/O”. One of the nicest things about working at the command line level is the ability to redirect input and output. For example, instead of typing input to a program with the keyboard, it can be read from a file using the symbol <. Output can either be printed to the screen (standard output), redirected into a file using the symbol >, appended to the end of a file with >> or used as input to another program with the pipe operator ()|.

4.5 Text editors

There are many ways of editing text and the subject is beyond the scope of this documentation. Text editing is a blessing and a curse. You either love it or hate it and in the beginning, and if you are used to programs like Word, you will certainly hate it. (And if you are used to a decent text editor, you will hate Word!). But you can't use Word because the output is in a weird format that no scripting languages read easily. So you have to use an editor that will produce a plain (ascii) file, like Notepad, TextWrangler or

Sublime Text. TextWrangler is freeware available for Macs and the notepad comes standard in the Windows operating system. Fortunately for Mac users, Enthought Python's Canopy programming environment comes with its own text editor.

Chapter 5

The PmagPy software package

The **PmagPy** software package is a comprehensive set of programs for paleomagnetists and rock magnetists. For installation, follow the instructions in the Installing PmagPy Chapter in this cookbook.

When you type something on your command line, your operating system looks for programs of the same name in special places. These are special “paths” so the directory with your Python scripts has to “be in your path”. To inform the operating system of the new directory, you need to “set your path”. It should have been set when you installed **PmagPy**.

5.1 Graphical data analysis programs

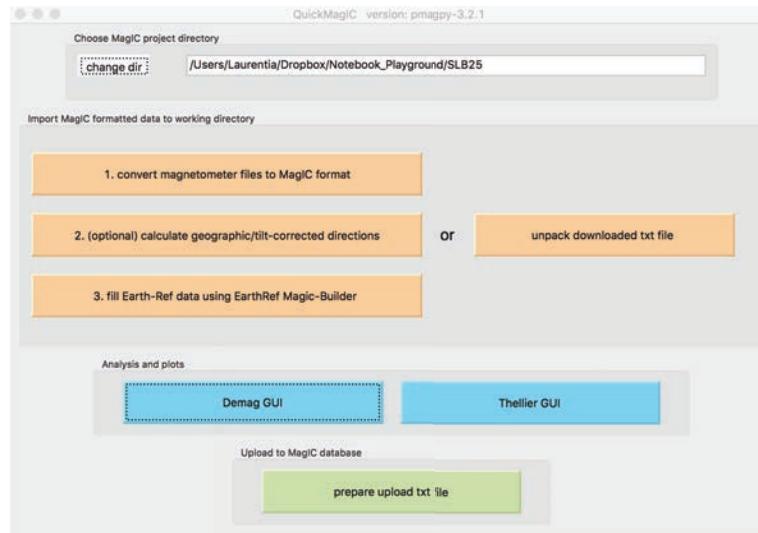
5.1.1 demag_gui.py

The Demag GUI (**demag_gui.py**) program enables the display and analysis of paleomagnetic demagnetization data. The software will display specimen level data within the chosen directory as a Zijderveld plot, equal area plot and intensity plot. Interpretations can be made to the data as least-squares line or plane fits. Mean directions can be calculated and displayed for these interpretations. These interpretations can be exported as MagIC pmag files from the program.

Launching

The best way to launch the Demag GUI application is through Pmag GUI. If PmagPy has been added to your PATH you can type `pmag_gui.py` at the

command line to launch it or you can navigate to the directory containing it and type `python ./pmag_gui.py`. Within Pmag GUI, data can be converted from the format of a particular lab into MagIC format so that it can be displayed and analyzed within Demag GUI. The program can be started by clicking on the Demag GUI button in Pmag GUI.



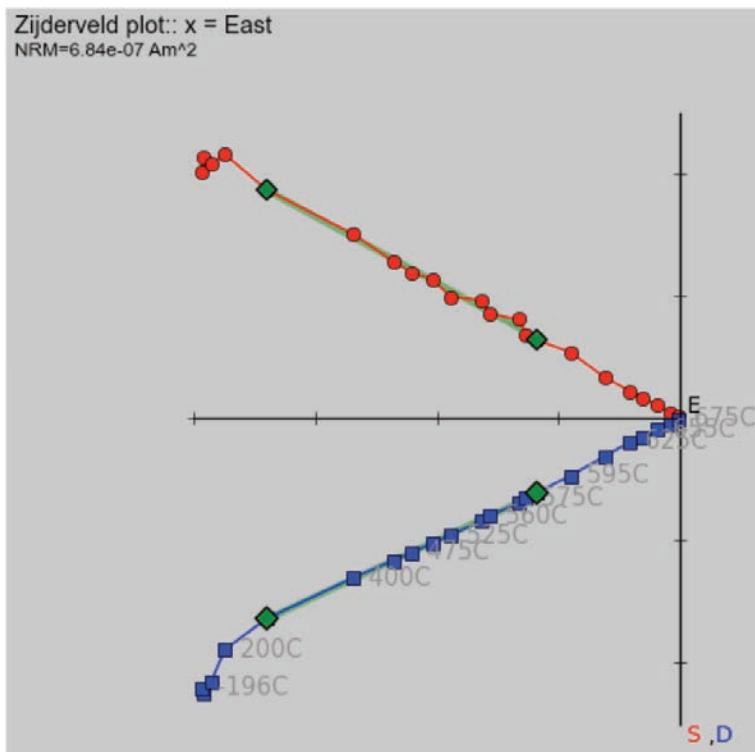
Demag GUI can also be launched through the command line by navigating to the directory containing `demag_gui.py` and running it with:

```
% python ./demag_gui.py
```

Or if **PmagPy** was properly installed and has been added to your PATH, you can simply type `demag_gui.py` at the command line. **Note:** on OSX it is recommended to launch through Pmag GUI as on wxpython 2.9 the drop-down boxes behave better when **Demag GUI** is launched this way.

Adding Interpretations:

A least-squares fit to the measurement data can be added by clicking the ‘add fit’ button. Additionally, you can select the fit you would like to edit or view by using the drop-down menu under the add fit button. Once you have selected a fit, the shape of the end points of the selected fit will turn to diamond shapes to distinguish them from the other data points.



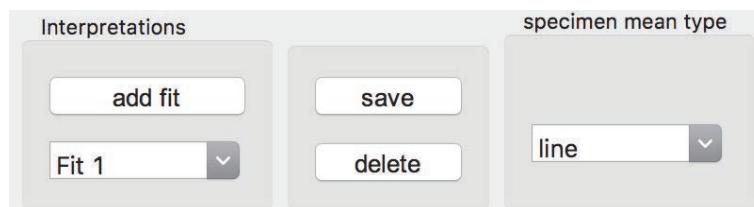
Once the desired fit is selected, its bounds can be edited using the drop-down boxes under the bounds header.



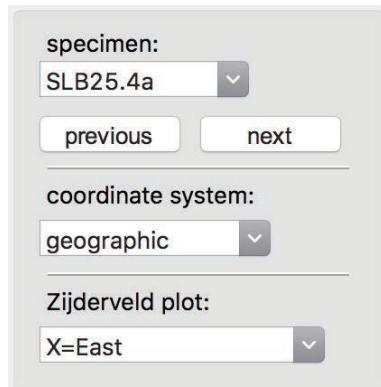
Another way to select bounds is to double-click the list of measurement steps on the left to pick out the bounds for the interpretation. The included steps in the currently selected interpretation are shown in highlighted in blue on the measurement list and the measurements marked “bad” are shown in highlighted in red. In the case of duplicate measurements, the first *good* measurement with the same treatment is used. All points between the selected bounds that are flagged good (i.e. not flagged bad and marked in red), including duplicate measurements, will be included in the interpreted fit..

i	Step	Tr	Dec	Inc	M
0	N	0.0	298.6	26.7	6.84e-0
1	T	-196.0	297.2	26.6	6.75e-0
2	T	100.0	298.4	26.2	6.68e-0
3	T	200.0	300.0	23.7	6.45e-0
4	T	300.0	298.9	22.9	5.77e-0
5	T	400.0	299.3	23.0	4.58e-0
6	T	450.0	298.6	23.5	4.00e-0
7	T	475.0	298.4	23.7	3.75e-0
8	T	500.0	299.3	23.7	3.49e-0
9	T	525.0	297.8	24.2	3.20e-0
10	T	550.0	300.7	23.8	2.83e-0
11	T	560.0	298.5	24.2	2.68e-0
12	T	570.0	301.4	23.9	2.33e-0
13	T	575.0	298.5	24.4	2.17e-0
14	T	580.0	298.5	24.4	2.01e-0
15	T	595.0	300.9	24.1	1.58e-0
16	T	610.0	298.4	23.8	1.05e-0
17	T	625.0	298.3	22.3	6.94e-0
18	T	640.0	298.2	23.9	5.29e-0

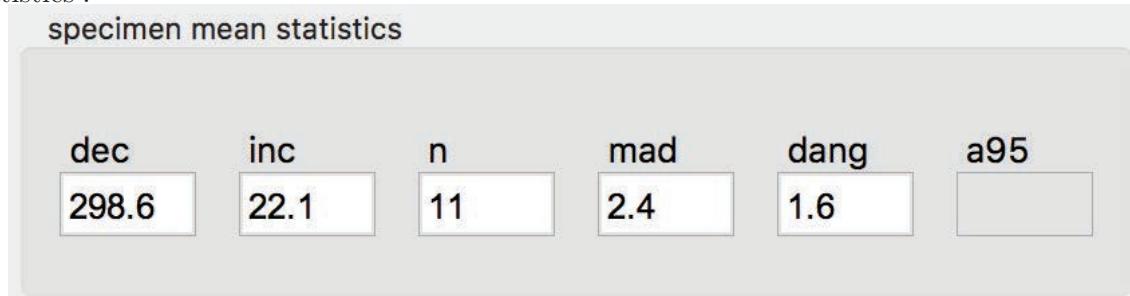
When first created, the fit will be given a generic name such as *Fit 1*. The name of the fit can be changed from the default by typing into the drop-down box containing fit name and then pressing enter. The default fit type is a least-squares line. You can choose different fits, such as a line anchored to the origin or a plane, by using the drop-down menu under the label ‘interpretation type’. Plane fits can be plotted as either poles, full planes or partial planes. This display option can be changed in the second drop-down menu under specimen mean type.



The choice between coordinate systems (i.e. specimen, geographic or tilt-corrected) is available on the left above the list of steps. The data list and the plots will update to reflect the chosen coordinate system.



The properties of the currently selected fit to the data can be seen in the upper center of the GUI in a box labeled ‘interpretation directions and statistics’.



Flagging Bad Measurement Data

Due to flux jumps or other such errors, individual measurements should sometimes be excluded from interpretation. Such a measurements can be flagged as “bad” by right-clicking them within the measurement list and the measurement will then be highlighted in red. The measurement_flag in the magic_measurements file will be change from “g” to “b” when a measurement is marked as “bad” and the step will not be included in fits that are made to the data. Any measurement marked as ‘bad’ will be colored red in the step list and will be shown as an empty rather than filled circle on the Zijderveld, equal area and M/M₀ plots. To change a ‘bad’ measurement back to being ‘good’, one can right click on it again. Upon doing so, the red highlighting will go away, the data will be shown colored in within the plots and any fit that spans that data point will be recalculated to include it.

Acceptance criteria can be set by using Analysis/“Acceptance Criteria”/“Change Acceptance Criteria”. These criteria will be written to a *pmag_criteria.txt* table.

Plot Interface

The four plots that take up the majority of the center of the GUI are where data and their interpretations are displayed. The Zijderveld and the two equal area plots are by default set to zoom when you left click and drag your left mouse button you will zoom to the dragged out rectangle(currently equal area plots do not draw this rectangle as you drag your mouse, but still zoom). On the Zijderveld plot, it is possible to switch between zoom and pan functionality by right clicking. Once in pan mode, the mouse will turn into a hand allowing you then to click and move around the plot. On both the Zijderveld and equal area plots if you wish to return to the original plot simply click the middle mouse button to return to home position. **Note:** in the absence of a middle mouse button pressing both right and left mouse buttons at the same time works on most laptops in the case of Macbooks clicking with two fingers should work, and if using Apple's magic mouse we recommend you download the MagicPrefs program which will allow you to configure your mouse however you prefer. One the equal area plots you can double click on an interpretation to switch the specimen and current interpretation to the clicked interpretation.

Saving Specimen Interpretations

Once you have picked out your interpretations, you can save the session data in two different ways: (1) as a .redo file which will allow you to have the fits preserved to be view again with Demag GUI or (2) as MagIC *pmag_** tables to be uploaded to the MagIC database or otherwise processed. In addition, you may save image files of the plots.

The .redo File: You can use Analysis/“Save current interpretations to a redo file” to create this file type or you can just hit the save button next to add fit. **Note:** this file type does **NOT** load previous interpretations on start up you must go to the menu option Analysis/“Import previous interpretations from a redo file” to restore your previous session.

The Pmag Tables: By going to the menu File/“Save MagIC pmag tables” you can export your interpretations made in Demag GUI to the MagIC pmag tables which can then be used by other MagIC programs or uploaded to the MagIC database. You can export any or all of the three coordinate systems upon selecting this option and you may choose to save *pmag-samples*, *pmag-sites*, and *pmag-results* tables in addition to the *pmag-specimens*

table that is output. If you choose to output additional information you will be prompted by a pop up window for additional information. **Note:** this save format loads on start up of the GUI immediately restoring your session. Selection of this option will overwrite your *demag_gui.redo* file in the working directory.

Images of Plots: Select the menu option File/“Save plot”/“Save all plots” to save all plots. Or, you can save any of the plots individually. If you zoom on any of the plots the zoomed image will be saved not the originally plotted image although the plot will redraw and reset the zoom level.

Deleting Specimen Interpretations

If you would like to delete a single interpretation, select the one you wish to delete from the interpretation drop-down menu and click delete. If you wish to clear all interpretations you may go into the interpretation editor located under the tools menu, select the fits you wish to delete and click the “delete selected” button.

Higher Level Plots and Interpretation

The set of drop-down boxes to the right of the interpretation data are there to determine what level you want to analyze in the higher level analysis options include: site, sample, location, and study. The drop-down below this selects which of the available sites, samples, location, or studies to display.

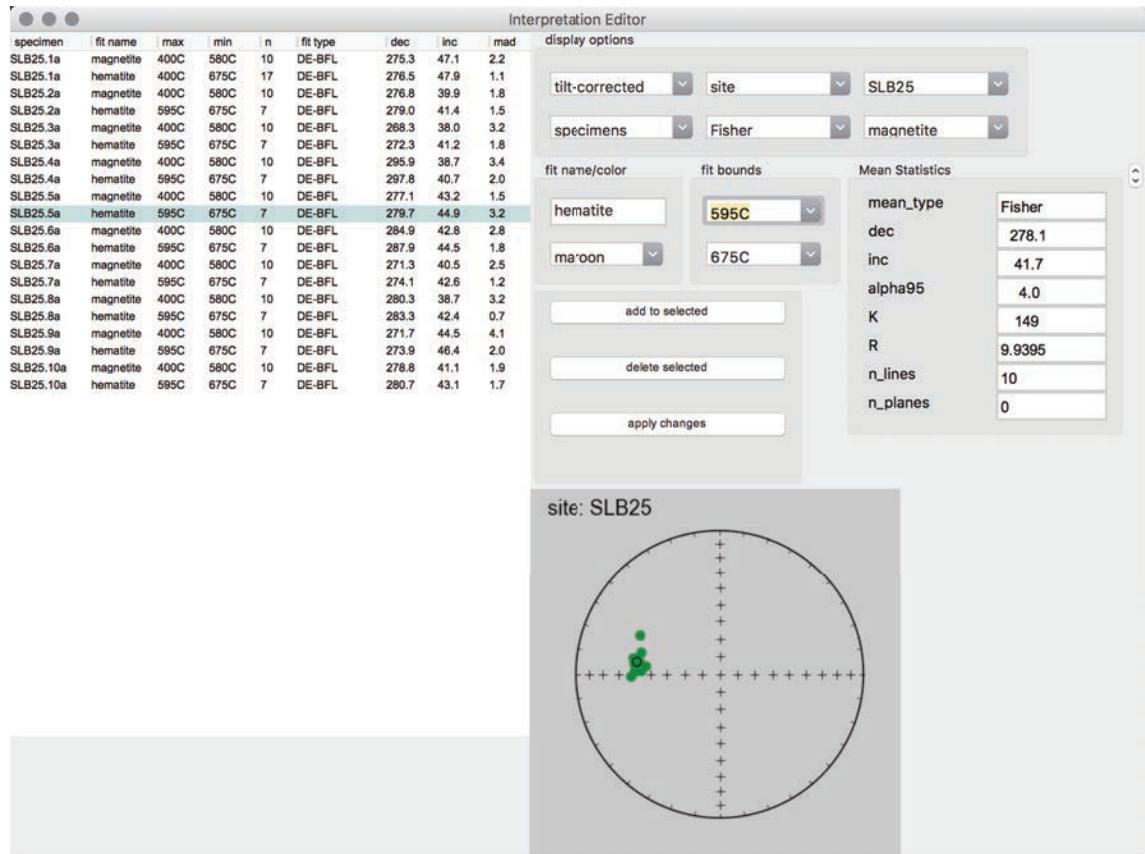
You can then select how to group your data by using the drop-down menu under the show header. You can select what kind of mean to take using the first drop-down under the mean header. Which interpretations to use for the means can be selected under the second drop-down menu.

The mean statistics for the chosen higher level mean are displayed in the lower right of the GUI.

Interpretation Editor

In order to more easily view and edit specimen interpretation data there is a specimen interpretation editor which can be launched from the tools menu. This panel details the fits made to the data and their parameters from which you can select which interpretation to view by double clicking on it. In the list, the currently selected interpretation is highlighted blue as shown

in the image below. You can mark interpretations as bad which removes them from any Fisher means or other high level means by right clicking on their entry in the list. All interpretations marked bad are colored red in the list and marked as an ‘x’ on the plot. The specimen entry associated with this fit will be given a bad (‘b’) flag within the pmag_specimens table. Interpretations can be highlighted by clicking on the list and holding the shift or ctrl/command key to select multiple interpretations. Doing so allows you to delete or alter the characteristics of multiple interpretations at once without having to select each one in turn. This mass alteration is allowable using the Name/Color/Bounds boxes to input the changes and then clicking the “apply changes to highlighted fits” button. You can delete highlighted fits using the “delete highlighted fits” button. The “add fit” button in the interpretation editor adds a fit to the current specimen. In the case of interpreting large data sets, you can reduce the number of items plotted on the equal area at the bottom of the editor and the number of entries in the log by changing the display settings.



5.1.2 thellier_gui.py

[Essentials Chapter 10] and [MagIC] [Thellier_GUI_full_manual.pdf]

The program Thellier GUI (**thellier_gui.py**) combines functions from `thellier_magic.py` and new tools described by Shaar and Tauxe (2013) in a user-friendly graphical user interface (GUI).

As with , Thellier GUI can be called from the command line or from within Pmag GUI. It loads files already prepared in a This Project directory and the interpretations from Thellier GUI are part of the workflow of Pmag GUI. This section is a brief introduction on how to use Thellier GUI as a stand alone application. Much more information is available within this manual: Thellier GUI full manual.

A complete list of the definitions for paleointensity statistics used by Thellier GUI is available as a supplement to the article by Paterson et al., 2014 and available for download here:

<http://onlinelibrary.wiley.com/store/10.1002/2013GC005135/asset/supinfo/ggge20412-sup-1.pdf>

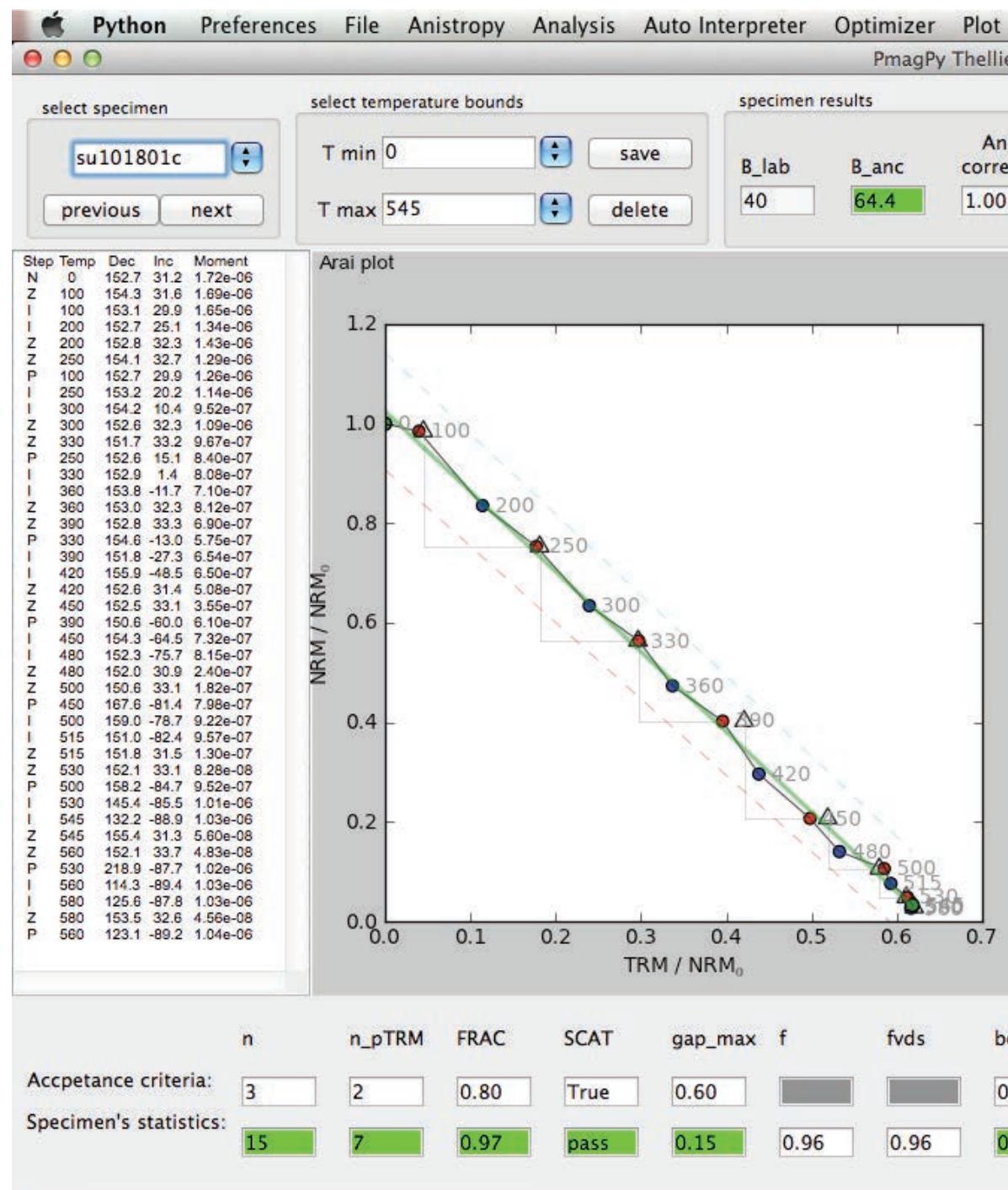
After launching the program, a “choose project directory” dialog window will appear as soon as the GUI is started. Your ThisProject directory should include a file named *magic_measurements.txt* (created for example by **Pmag GUI**). If a file named *rmag_anisotropy.txt* is in the project directory, then the program reads in the anisotropy data. Reading and processing the measurements files may take several seconds, depending on the number of the specimens.

Reading and compiling measurements data

When your ThisProject project directory is selected, the program reads all the measurement data, checks them, processes them and sorts them. If non-linear-TRM (NLT) data exist in *magic_measurement.txt* then the program tries to process the data using Equations (1)-(3) in Shaar et al., 2010. The program reads *magic_measurement.txt*, and processes the measurements for presentation as Arai and Zijderveld plots. We recommend that you check all the warnings and errors in *Thellier_GUI.log* before starting to interpret the data. For details about warnings and error messages during these steps, consult the tutorial document in the *thellier_GUI* folder in *data_files*. Also, consult the Preferences to change certain plotting options.

Main panel

This figure shows a snapshot of the main panel.



The top field in the panel includes the following buttons/controls (from left to right):

- **Specimen:** a list of the specimens in the project folder sorted by name.
- **previous/next:** buttons to move forward and backward in the specimens list.
- **T min/T max:** buttons to select temperature bounds.
- **save/delete:** save or delete current interpretation. This information will be used later to generate a redo file.
- **B_lab:** laboratory field in units of μT .
- **B_anc:** specimen's paleointensity in units of μT .
- **Aniso Correction:** anisotropy correction factor.
- **NLT Correction:** Non-Linear TRM (NLT) correction factor.
- **Dec/Inc:** Specimen declination/inclination calculated by PCA of the NRM in the selected temperature bounds.
- Sample mean, number of specimens, standard deviation and percent standard deviation.

The center of the main panel has these elements:

- **measurements text panel:** Four columns of the measurement data: Step is "N" for NRM, "Z" for zero field step, "I" for infield step, "P" for pTRM check, and "T" for tail check. The temperature of each step is given in C. Also shown declination, inclination and moment (in units of Am^2)
- **Arai plot:** Arai plot normalized by NRM_0 . blue circles are zero field steps, red circles are infield steps, triangles are pTRM checks, blue squares are tail checks. Temperatures are displayed near data points. Temperature bounds and best fit line are marked in green. 'SCAT box' is marked with dashed lines (only if SCAT is True).
- **Zijderveld plot:** A Zijderveld plot of the NRM step. The x axis is rotated to the direction of the NRM, blue is the x-y projection, and red is x-z projection.

- **Equal area plot:** An equal area projections of the NRM steps. solid circles are positive inclination. open circles are negative inclinations.
- **Moment-temperature plot:** NRMs are in blue, pTRMs are in red.
- **sample data:** If at least two specimens have a saved interpretation, then their values are displayed on this plot. The mean \pm standard deviation of the mean are marked as horizontal lines.

The bottom of the main panel include paleointensity statistics. The first line has the threshold values (empty if N/A). The second line is the specimen's statistics. For details see Appendix A1 in Shaar and Tauxe (2013).

5.1.3 MagIC GUI

This application provides a simple interface for transforming data from a paleomagnetic or rock magnetic study into the format necessary for contribution to the MagIC database.

5.2 Command line PmagPy programs

PmagPy scripts work by calling them on a command line. The python scripts must be placed in a directory that is in your “path”. To see if this has been properly done, type **dir_cart.py -h** on the command line and you should get a help message. If you get a “command not found” message, you need to fix your path; check the “installing python” page on the software website. Another possible cause for failure is that somehow, the python scripts are no longer executable. To fix this, change directories into the directory with the scripts, and type the command: **chmod a+x *.py**

For people who hate command line programs and prefer graphical user interfaces with menus, etc., some of the key programs for interpreting paleomagnetic and rock magnetic data are packaged together in a program called Pmag GUI. This can be invoked by typing **pmag-gui.py** on the command line. The Pmag GUI program generates the desired commands for you behind the scenes, so you do not have to learn UNIX or how to use the command line (except to call **Pmag GUI** itself). Nonetheless, some understanding of what is actually happening is helpful, because **Pmag GUI** is more limited than full range of **PmagPy** programs. So, here is a brief introduction to how the **PmagPy** programs work.

All **PmagPy** programs print a help message out if you type: **program_name.py -h** on the command line. Many have an “interactive”

option triggered by typing **program_name.py -i**. Many also allow reading from standard input and output. The help message will explain how each particular program functions. There are some common features for the command line options:

- Switches are from one to three characters long, preceded by a '-'.
- The switch '-h' always prints the help message and '-i' allows interactive entry of options.
- Options for command line switches immediately follow the switch. For example: -f INPUT -F OUTPUT will set the input file to INPUT and the output to OUTPUT.
- The switch for input files all start with -f and -F for output files.
- -spc -sam -sit -syn -loc are switches relating to specimens, samples, sites, synthetics and locations respectively.
- Capitalized switches suppress an option (e.g., -A means do not average, while -a means DO average).
- -crd [s,g,t] sets the coordinate system
- -fmt [svg,png,jpg] the default image format.
- -sav saves the plots silently and quits the program

The **PmagPy** scripts call on two special modules, the **pmag** and the **pmagplotlib** modules. These contain most of the calculations and plotting functions.

The source code and the help messages for all programs in the PmagPy package are also available online at:

<https://github.com/PmagPy/PmagPy>

A link to these source code/help menu files is provided for each program listed below with the format [program_name_docs].

Examples of how to use command line **PmagPy** programs are given below. In all examples, the '\$' prompt stands for whatever command line prompt you have. The example data files referred to in the following are located in the *data_files* directory bundled with the **PmagPy** software distribution.

5.2.1 aarm_magic.py

[Essentials Chapter 13] [MagIC Database] [aarm_magic docs]

Anisotropy of anhysteretic or other remanence can be converted to a tensor and used to correct natural remanence data for the effects of anisotropy remanence acquisition. For example, directions may be deflected from the geomagnetic field direction or intensities may be biased by strong anisotropies in the magnetic fabric of the specimen. By imparting an anhysteretic or thermal remanence in many specific orientations, the anisotropy of remanence acquisition can be characterized and used for correction. We do this for anisotropy of anhysteretic remanence (AARM) by imparting an ARM in 9, 12 or 15 positions. Each ARM must be preceded by an AF demagnetization step. The 15 positions are shown in the k15_magic.py example.

For the 9 position scheme, **aarm_magic.py** assumes that the AARMs are imparted in positions 1,2,3, 6,7,8, 11,12,13. Someone (a.k.a. Josh Feinberg) has kindly made the measurements and saved them an SIO formatted measurement file named *arm-magic-example.dat* in the datafile directory called *aarm-magic*. Note the special format of these files - the treatment column (column #2) has the position number (1,2,3,6, etc.) followed by either a “00” for the obligatory zero field baseline step or a “10” for the in-field step. These could also be ‘0’ and ‘1’.

We need to first import these into the *magic-measurements* format and then calculate the anisotropy tensors. These can then be plotted or used to correct paleointensity or directional data for anisotropy of remanence.

So, first use the program **sio_magic.py** to import the AARM data into the MagIC format. The DC field was 50 μ T, the peak AC field was 180 mT, the location was ‘Bushveld’ and the lab protocol was AF and Anisotropy. The naming convention used Option # 3 (see help menu).

Then use the program **aarm_magic.py** to calculate the best-fit tensor and write out the MagIC tables: *rmag_anisotropy* and *rmag_results*. These files can be used to correct remanence data in a *pmag-specimens* format table (e.g, intensity data) for the effects of remanent anisotropy (e.g., using the program **thellier_magic_redo.py**).

Here is a transcript of a session that works. Note that the **sio_magic.py** command is all on one line (which is what the terminal backslash means).

```
$ sio_magic.py -f arm_magic_example.dat -loc Bushveld -LP AF:ANI -F aarm_measurements
      -ncn 3 -ac 180 -dc 50 -1 -1
      results put in aarm_measurements.txt
```

```
$ aarm_magic.py
specimen tensor elements stored in ./arm_anisotropy.txt
specimen statistics and eigenparameters stored in ./aarm_results.txt
```

5.2.2 angle.py

[Essentials Appendix A.3.4] [angle docs]

Use the program **angle.py** to calculate the angle (α) between two directions $D = 350.2, I = 26.8; D = 98.6, I = 67.3$.

```
$ angle.py -i
Declination 1: [cntrl-D  to quit] 350.2
Inclination 1: 26.8
Declination 2: 98.6
Inclination 2: 67.3
    72.1
Declination 1: [cntrl-D  to quit] ^D
Good bye
```

[NB: PC users will get a more angry sounding exit message]

You can also use this program by reading in a filename using the '-f' option or from standard input (with <). Try this out with the test file in the *angle* directory (*angle.dat*). First examine the contents of the input file using “**cat**” (or “**type**” on a DOS prompt). Then use **angle.py** to calculate the angles. You can also save your output in a file *angle.out* with the '-F' option:

```
$ cat angle.dat
  11.2    32.9      6.4   -42.9
  11.5    63.7     10.5   -55.4
  11.9    31.4    358.1   -71.8
 349.6    36.2    356.3   -45.0
   60.3    63.5     58.9   -56.6
 351.8    37.6     55.0   -45.8
 345.5    53.1     44.8   -26.9
   12.2    20.1     13.6   -54.0
 352.1    37.6      5.1   -39.9
 341.2    53.8     25.1   -61.1
```

```

.....
$ angle.py -f angle.dat
 75.9
119.1
103.7
 81.4
120.1
100.9
 95.1
 74.1
 78.4
120.1
.....
.
.
```

5.2.3 ANI_depthplot.py

[Essentials Chapter 13]; [MagIC Database] [ANI_depthplot docs]

Anisotropy data can be plotted versus depth. The program **ANI_depthplot.py** uses MagIC formatted data tables of the *rmag_anisotropy.txt* and *er_samples.txt* types. *rmag_anisotropy.txt* stores the tensor elements and measurement meta-data while *er_samples.txt* stores the depths, location and other information. Bulk susceptibility measurements can also be plotted if they are available in a *magic_measurements.txt* formatted file.

In this example, we will use the data from Tauxe et al. (2012) measured on samples obtained during Expedition 318 of the International Ocean Drilling Program. To get the entire dataset, go to the MagIC data base at: <http://earthref.org/MAGIC/> and find the data using the search interface. As a short-cut, you can use the “permalink”:

<http://earthref.org/MAGIC/m000629dt20120607193954>.

Download the text file by clicking on the icon under the red arrow in:

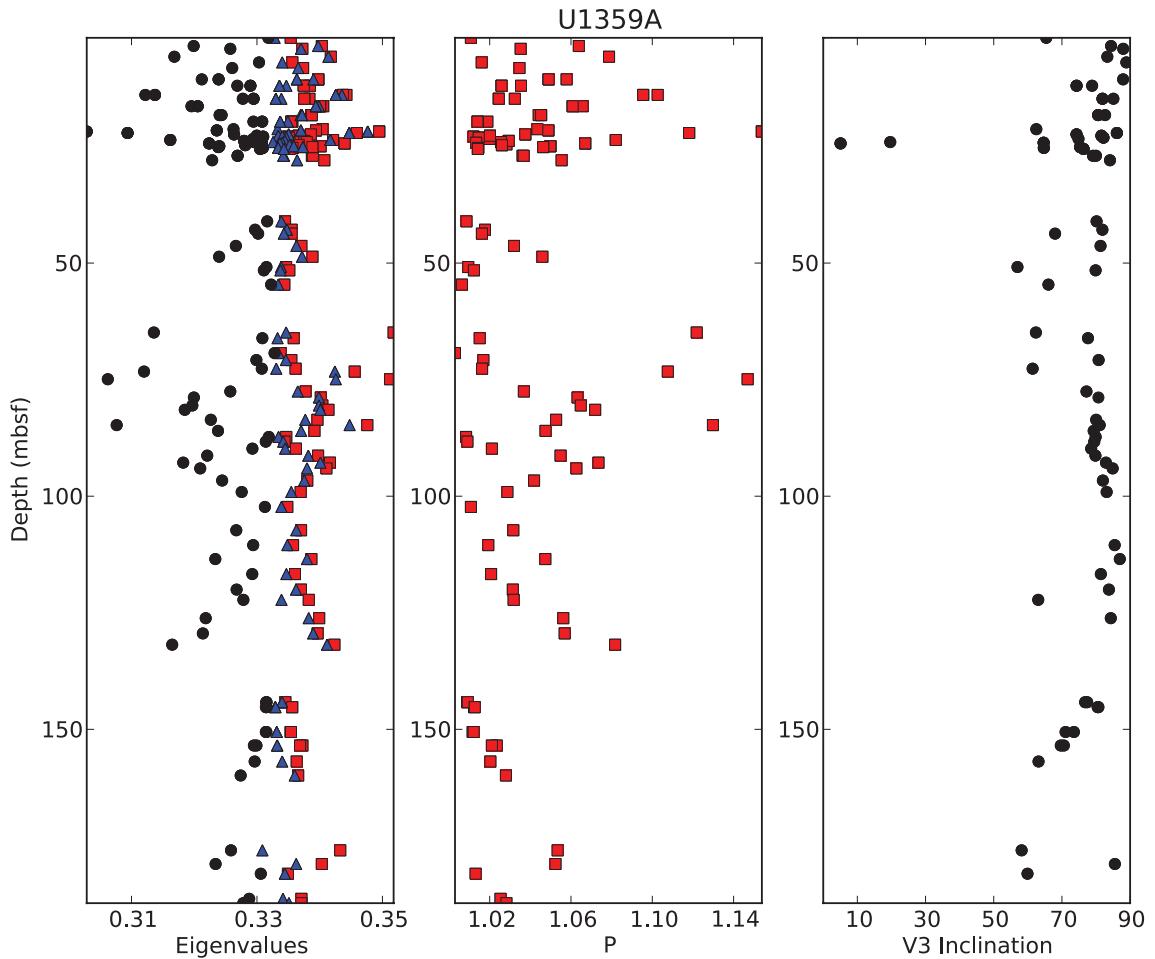
The screenshot shows a search results page from EarthRef.org. The top navigation bar includes 'Home', 'Data' (which is selected), 'Maps', and 'Plots'. A search bar at the top right says 'Search for a reference (e.g. "Tauxe and 2003").' Below the search bar is a header with links for 'Contribution (1)', 'Location (6)', 'Site (17,098)', 'Sample (17,098)', 'Specimen (17,098)', and 'Measurement (33,113)'. The main table has columns for 'Contribution', 'Records', 'Contributor Actions', 'DOI Link', 'Contribution SmartBook', and 'Full Reference'. A 'Save Results' button, a 'Search Filters (1)' button, and a 'Show Empty Columns (10)' link are at the bottom left of the table. A message 'Retrieved 1 row out of 1 match' is at the bottom right. The single result row for 'Tauxe et al. (2012)' contains the following information:

Tauxe et al. (2012) by Lisa Tauxe (Original Author) on 07 Jun 2012 (ver. 1) http://earthref.org/MAGIC/m000629d/20120607193954	6 Locations 17098 Sites 17098 Samples 19100 Measurements 33113 Measurements	Update	doi>	[CSV icon]	[Text file icon] click here to download text file	Tauxe, L., Stickley, C.E., Sugisaki, S., Bijl, P.K., Bohaty, S.M., Brinkhuis, H., Escutia, C., Flores, J.-A., Houben, A.J.P., Iwai, M., Jimenez-Espejo, F., McKay, R., Passchier, S., Pross, J., Rieselman, C.R., Roehl, U., Sangiorgi, F., Welsh, K., Klaus, A., Fehr, A., Bendle, J.A.P., Dunbar, R.B., Gonzalez, J., Hayden, T., Katsuki, K., Olney, M., Pekar, S.F., Shrivastava, P.K., van de Flierdt, T., Williams, T. and Yamane, M. (2012). Integrated biomagnetostratigraphy of the Wilkes Land Margin for reconstruction of 53 Ma of Antarctic. <i>Paleoceanography</i> 1-10. doi: 10.1029/2012PA002308.
--	---	------------------------	-------------------------	----------------------------	---	---

Unpack the data using the program `download_magic.py`. This will unpack the data into the different holes. Change directories into `Location_2` (which contains the data for Hole U1359A). Or, you can use the data in the `ANI_depthplot` directory of the example data files.

```
$ ANI_depthplot.py
```

will create the plot:



5.2.4 aniso_magic.py

[Essentials Chapter 13]; [MagIC Database] [aniso_magic docs]

Samples were collected from the eastern margin a dike oriented with a bedding pole declination of 110° and dip of 2° . The data have been imported into a rmag_anisotropy formatted file named *dike_anisotropy.txt*.

Make a plot of the data using **aniso_magic.py**. Use the site parametric bootstrap option and plot out the bootstrapped eigenvectors. Draw on the trace of the dike.

These things are done in this session:

```
$ aniso_magic.py -f dike_anisotropy.txt -gtc 110 2 -par -v -crd g
Doing bootstrap - be patient
```

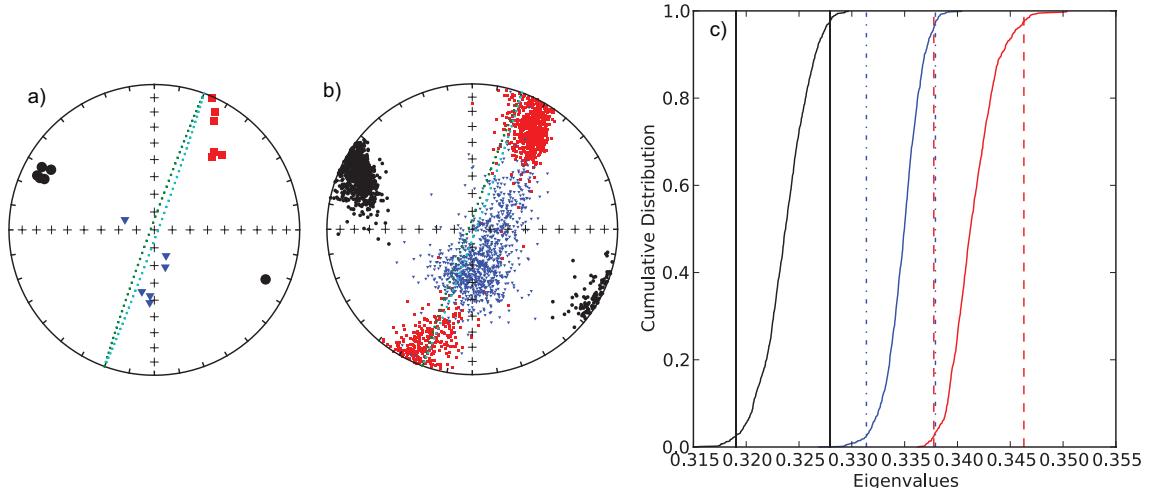
Bootstrap Statistics:

tau_i, V_i_D, V_i_I, V_i_zeta, V_i_zeta_D, V_i_zeta_I, V_i_eta, V_i_eta_D, V_i_eta_I								
0.34040287	29.6	14.5	6.9	168.4	67.4	32.7	295.9	14.2
0.33536589	166.3	70.5	10.3	26.1	13.0	23.9	293.3	12.1
0.32423124	296.2	12.8	5.2	180.5	62.4	10.4	32.0	24.0

compare with [d]irection

plot [g]reat circle, change [c]oord. system, change [e]llipse calculation,
s[a]ve plots, [q]uit

which produced these plots:



The specimen eigenvectors are plotted in the left-hand diagram with the usual convention that squares are the V_1 directions, triangles are the V_2 directions and circles are the V_3 directions. All directions are plotted on the lower hemisphere. The bootstrapped eigenvectors are shown in the middle diagram. Cumulative distributions of the bootstrapped eigenvalues are shown to the right with the 95% confidence bounds plotted as vertical lines. It appears that the magma was moving in the northern and slightly up direction along the dike.

There are more options to **aniso_magic.py** that come in handy. In particular, one often wishes to test if a particular fabric is isotropic (the three eigenvalues cannot be distinguished), or if a particular eigenvector is parallel to some direction. For example, undisturbed sedimentary fabrics are oblate (the maximum and intermediate directions cannot be distinguished from one another, but are distinct from the minimum) and the eigenvector associated with the minimum eigenvalue is vertical. These criteria can be

tested using the distributions of bootstrapped eigenvalues and eigenvectors.

The following session illustrates how this is done, using the data in the test file `sed_anisotropy.txt` in the `aniso_magic` directory.

```
$ aniso_magic.py -f sed_anisotropy.txt -d 3 0 90 -v -crd g
```

Doing bootstrap - be patient

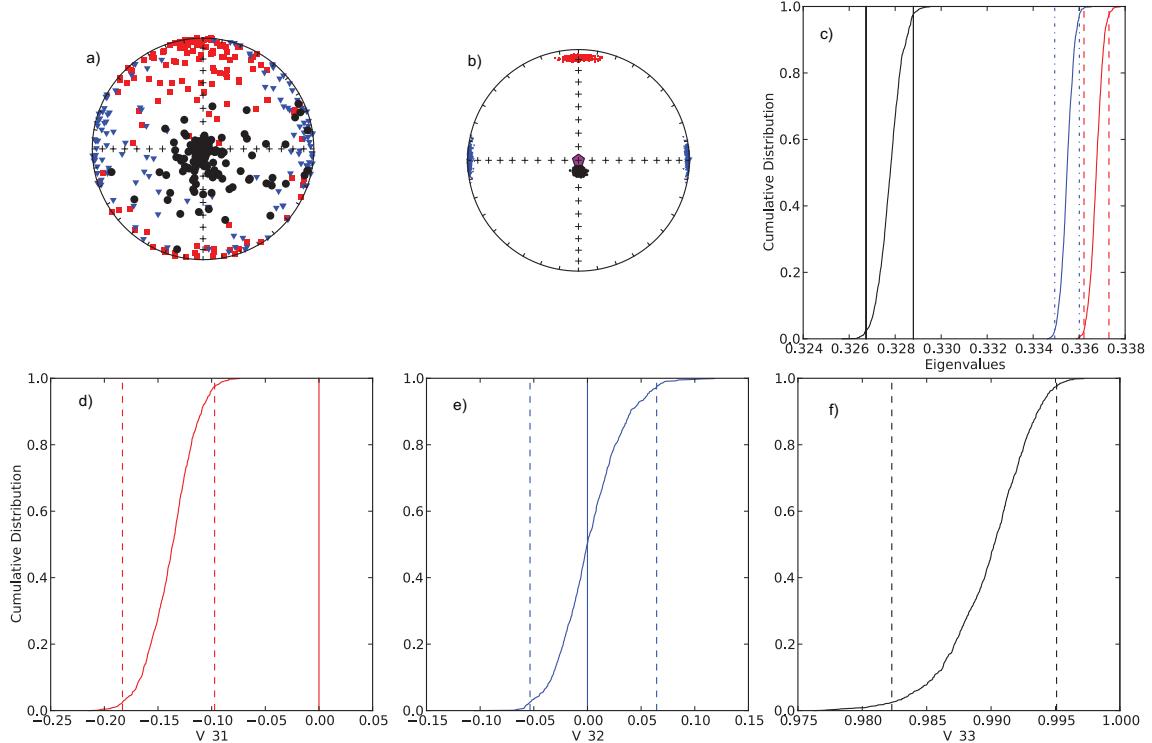
Bootstrap Statistics:

$\tau_{i,i}$	$V_{i,D}$	$V_{i,I}$	$V_{i,\zeta}$	$V_{i,\zeta,D}$	$V_{i,\zeta,I}$	$V_{i,\eta}$	$V_{i,\eta,D}$	$V_{i,\eta,I}$
0.33673453	359.5	7.9	9.8	156.0	81.6	3.2	269.3	3.3
0.33546972	89.5	0.0	37.5	11.5	53.7	80.3	178.0	35.5
0.32779574	179.6	82.1	4.1	4.7	7.6	3.2	274.6	1.2

compare with [d]irection

plot [g]reat circle, change [c]oord. system, change [e]llipse calculation,
s[a]ve plots, [q]uit

which makes these plots:



The top three plots are as in the dike example before, showing a clear triaxial fabric (all three eigenvalues and associated eigenvectors are distinct

from one another. In the lower three plots we have the distributions of the three components of the chosen axis, V_3 , their 95% confidence bounds (dash lines) and the components of the designated direction (solid line). This direction is also shown in the equal area projection above as a red pentagon. The minimum eigenvector is not vertical in this case.

5.2.5 apwp.py

[Essentials Chapter 16] [apwp docs]

The program **apwp.py** calculates paleolatitude, declination, inclination from a pole latitude and longitude based on the paper Besse and Courtillot (2002; see Essentials Chapter 16 for complete discussion). Use it to calculate the expected direction for 100 million year old rocks at a locality in La Jolla Cove (Latitude: 33N, Longitude 117W). Assume that we are on the North American Plate! (Note that there IS no option for the Pacific plate in the program **apwp.py**, and that La Jolla was on the North American plate until a few million years ago (6?).

```
$ apwp.py -i

Welcome to paleolatitude calculator - CTRL-D to quit

pick a plate: NA, SA, AF, IN, EU, AU, ANT, GL

Plate
NA
Site latitude
33
Site longitude
-117
Age
100
Age  Paleolat.  Dec.  Inc.  Pole_lat.  Pole_Long.
100.0    38.8   352.4    58.1    81.5   198.3
```

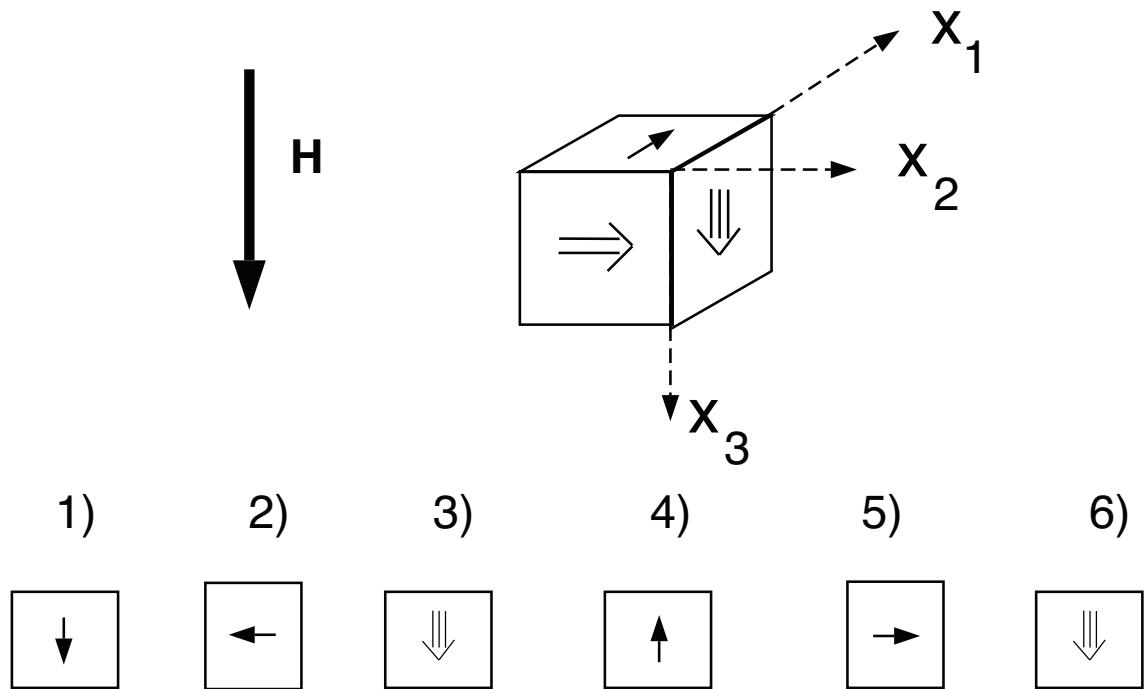
Note that as with many **PmagPy** programs, the input information can be read from a file and the output can be put in a file. For example, we put the same information into a file, *apwp-example.dat* and use this syntax:

```
$ apwp.py -f apwp_example.dat
100.0    38.8   352.4    58.1    81.5   198.3
```

5.2.6 atrm_magic.py

[Essentials Chapter 13] [MagIC Database] [atrm_magic docs]

Anisotropy of thermal remanence (ATRM) is similar to anisotropy of anhysteretic remanence (AARM) and the procedure for obtaining the tensor is also similar. Therefore, the program **atrm_magic.py** is quite similar to **aarm_magic.py**. However, the SIO lab procedures for the two experiments are somewhat different. In the ATRM experiment, there is a single, zero field step at the chosen temperature which is used as a baseline. We use only six positions (as opposed to nine for AARM) because of the additional risk of alteration at each temperature step. The positions are also different:



The file *atrm_magic-example.dat* in the *atrm_magic* directory is an SIO formatted data file containing ATRM measurement data done in a temperature of 520°C. Note the special format of these files - the treatment column (column #2) has the temperature in centigrade followed by either a “00” for the obligatory zero field baseline step or a “10” for the first position, and so on. These could also be ‘0’ and ‘1’, etc..

Use the program *sio_magic.py* to import the ATRM data into the MagIC format. The DC field was 40 μ T. The naming convention used option # 1 (see help menu). Then use the program **atrm_magic.py** to calculate

the best-fit tensor and write out the MagIC tables: *rmag_anisotropy* and *rmag_results* formatted files. These files can be used to correct remanence data in a *pmag-specimens* format table (e.g., intensity data) for the effects of remanent anisotropy (e.g., using the program *thellier_magic_redo.py*.

Here is an example transcript:

```
$ sio_magic.py -f atrm_magic_example.dat -loc Africa -LP T:ANI -F atrm_measurements.txt
      -ncn 1 -dc 40 -1 -1

results put in atrm_measurements.txt

$ atrm_magic.py

specimen tensor elements stored in ./trm_anisotropy.txt
specimen statistics and eigenparameters stored in ./atrm_results.txt
```

5.2.7 azdip_magic.py

[Essentials Chapter 9] and [MagIC Database] [azdip_magic docs]

Many paleomagnetists save orientation information in files in this format: Sample Azimuth Plunge Strike Dip (AZDIP format), where the Azimuth and Plunge are the declination and inclination of the drill direction and the strike and dip are the attitude of the sampled unit (with dip to the right of strike). The MagIC database convention is to use the direction of the *X* coordinate of the specimen measurement system. To convert an *AzDip* formatted file (*example.az*) for samples taken from a location name “Northern Iceland” into the MagIC format and save the information in the MagIC *er_samples.txt* file format, use the program **azdip_magic.py**:

```
$ azdip_magic.py -f azdip_magic_example.dat -ncn 1 -mcd FS-FD:SO-POM
      -loc ‘‘Northern Iceland’’
```

Data saved in er_samples.txt

Note that there are many options for relating sample names to site names and we used the first convention that has a single character at the end of the site name to designate each sample (e.g., is132d is sample ’d’ from site is132). We have also specified certain field sampling and orientation method codes

(-mcd), here field sampling-field drilled (FS-FD) and sample orientation-Pomeroy (SO-POM). The location was “Northern Iceland”. See the help menu for more options.

Another way to do this is to use the `orientation_magic.py` program which allows much more information to be imported.

5.2.8 b_vdm.py

[Essentials Chapter 2] [b_vdm docs]

Use the program **b_vdm** to convert an estimated paleofield value of 33 μT obtained from a lava flow at 22° N latitude to the equivalent Virtual Dipole Moment (VDM) in Am^2 . Put the input information into a file called `vdm_input.dat` and read from it using standard input :

```
$ cat > b_vdm_example.dat
33 22
^D
$ b_vdm.py < b_vdm_example.dat
7.159e+22
```

5.2.9 basemap_magic.py

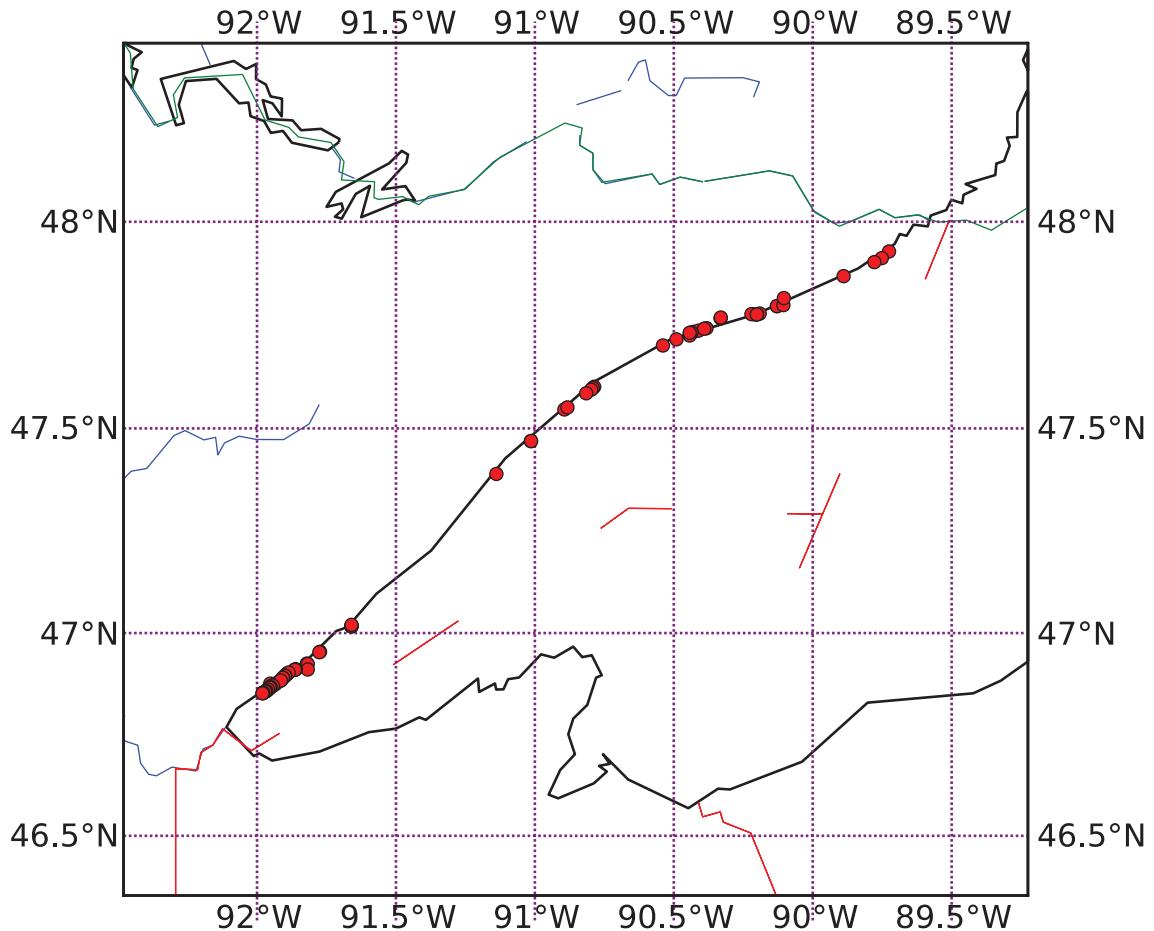
[MagIC Database] and high resolution instructions [basemap_magic docs]

NB: this program no longer maintained - use `plot_mapPTS.py` for greater functionality.

Python has a complete map plotting package and PmagPy has a utility for making simple base maps for projects. Site location data imported for example using `orientation_magic.py` into an `er_sites` formatted text file can be plotted using **basemap_magic.py**. There are many options, so check the help message for more details. Note that if you want to use high resolution datafiles or the etopo20 meshgrid (-etp option), you must install the high resolution continental outlines. You can use `install_etopo.py` for that. As an example, use the program **basemap_magic.py** to make a simple base map with site locations in a MagIC `er_sites.txt` formatted file named `basemap_example.txt`.

```
$ basemap_magic.py -f basemap_example.txt
```

which makes this plot:



Use the buttons at the bottom of the plot to resize or save the plot in the desired format.

5.2.10 biplot_magic.py

[Essentials Chapter 8] and [MagIC Database] [biplot_magic docs]

It is often useful to plot measurements from one experiment against another. For example, rock magnetic studies of sediments often plot the IRM against the ARM or magnetic susceptibility. All of these types of measurements can be imported into a single *magic_measurements* formatted file, using magic method codes and other clues (lab fields, etc.) to differentiate one from another. Data were obtained from a Paleogene core from 28°S for a relative paleointensity study. IRM, ARM, magnetic susceptibility and remanence data were uploaded to the MagIC database. The *magic_measurements*

formatted file for this study is saved in *core_measurements.txt*.

Use the program **biplot_magic.py** to make a biplot of magnetic susceptibility against ARM. Note that the program makes use of the MagIC method codes which are LT-IRM for IRM, LT-AF-I for ARM (AF demagnetization, in a field), and LP-X for magnetic susceptibility.

First, to find out which data are available, run the program like this:

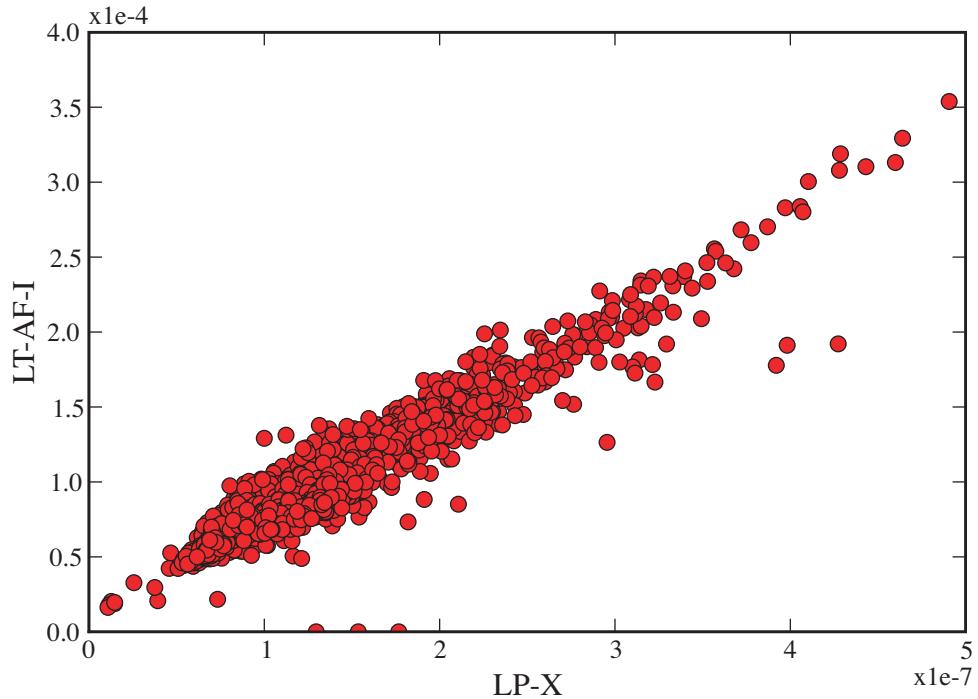
```
$ biplot_magic.py -f biplot_magic_example.txt
which responds with this:
['LT-AF-Z', 'LT-AF-I', 'LT-IRM', 'LP-X']
```

These are the method codes for AF demagnetization of NRM, ARM, IRM and susceptibility measurements respectively. So to make a plot of susceptibility against ARM, we would run the program again:

```
$ biplot_magic.py -f biplot_magic_example.txt -x LP-X -y LT-AF-I
LP-X selected for X axis
LT-AF-I selected for Y axis
All
measurement_magn_mass being used for plotting Y
measurement_chi_mass being used for plotting X.

S[a]ve plots, [q]uit, Return for next plot
```

which makes the plot:



5.2.11 bootams.py

[Essentials Chapter 13] [bootams docs]

The program **bootams.py** calculates bootstrap statistics for anisotropy tensor data in the form of:

`x11 x22 x33 x12 x23 x13`

It does this by selecting para-data sets and calculating the Hext average eigenparameters. It has an optional parametric bootstrap whereby the σ for the data set as a whole is used to draw new para data sets. The bootstrapped eigenparameters are assumed to be Kent distributed and the program calculates Kent error ellipses for each set of eigenvectors. It also estimates the standard deviations of the bootstrapped eigenvalues.

Use this to calculate the bootstrapped error statistics for the data in file `bootams_examples.data`:

```
$ bootams.py -par -f bootams_example.dat
Doing bootstrap - be patient
```

```

tau tau_sigma V_dec V_inc V_eta V_eta_dec V_eta_inc V_zeta V_zeta_dec V_zeta_inc

0.33505 0.00021      5.3     14.7    11.7    267.1    28.0    27.0    122.6    56.8
0.33334 0.00023     124.5    61.7    19.6    244.0    14.4    23.5    340.1    22.1
0.33161 0.00026     268.8    23.6    10.4     8.6    21.8    20.4    137.0    57.3

```

Note that every time bootams gets called, the output will be slightly different because this depends on calls to random number generators. If the answers are different by a lot, then the number of bootstrap calculations is too low. The number of bootstraps can be changed with the -nb option.

5.2.12 cart_dir.py

[Essentials Chapter 2] [cart_dir docs]

Use the program **cart_dir.py** to convert these cartesian coordinates to geomagnetic elements:

x_1	x_2	x_3
0.3971	-0.1445	0.9063
-0.5722	0.0400	-0.8192

To use the interactive option:

```
$ cart_dir.py -i
X: [cntrl-D to quit] 0.3971
Y: -0.1445
Z: 0.9063
340.0   65.0  1.000e+00
X: [cntrl-D to quit] -.5722
Y: 0.0400
Z: -0.8192
176.0   -55.0  1.000e+00
```

To read from a file:

```
$ cart_dir.py -f cart_dir_example.dat
340.0   65.0  1.000e+00
176.0   -55.0  1.000e+00
```

5.2.13 chartmaker.py

[Essentials Chapter 10] [chartmaker docs]

Paleointensity experiments are quite complex and it is easy to make a mistake in the laboratory. The SIO lab uses a simple chart that helps the experimenter keep track of in-field and zero field steps and makes sure that the field gets verified before each run. You can make a chart for an infield-zerofield, zerofield-infield (IZZI) experiment using the program **chartmaker.py**. Make such a chart using 50°C steps up to 500°C followed by 10°C steps up to 600°C.

```
$ chartmaker.py
Welcome to the thellier-thellier experiment automatic chart maker.
Please select desired step interval and upper bound for which it is valid.
e.g.,
50
500
10
600

a blank entry signals the end of data entry.
which would generate steps with 50 degree intervals up to 500,
followed by 10 degree intervals up to 600.

chart is stored in: chart.txt

Enter desired treatment step interval: <return> to quit 50
Enter upper bound for this interval: 500
Enter desired treatment step interval: <return> to quit 10
Enter upper bound for this interval: 600
Enter desired treatment step interval: <return> to quit
output stored in: chart.txt

%cat chart.txt
file:-----      field:-----uT

date | run# | zone I | zone II | zone III | start | sp |
-----|-----|-----|-----|-----|-----|-----|
0.0   |     |     |     |     |     |     |
-----|-----|-----|-----|-----|-----|-----|
Z    100.0 |     |     |     |     |     |     |
-----|-----|-----|-----|-----|-----|-----|
```

I	100.1					
<hr/>						
T	100.3					
<hr/>						
I	150.1					
.						
.						
.						

The chart allows you to fill in the file name in which the data were stored and the field value intended for the infield steps. The designations ‘Z’, ‘T’, ‘T’, and ‘P’ are for zero-field, in-field, pTRM tail checks and pTRM checks respectively. There are fields for the date of the runs, the fields measured in different zones in the oven prior to the start of the experiment, and the start and stop times. The numbers, e.g., 100.1 are the treatment temperatures (100) followed by the code for each experiment type. These get entered in the treatment fields in the SIO formatted magnetometer files (see `sio_magic.py`).

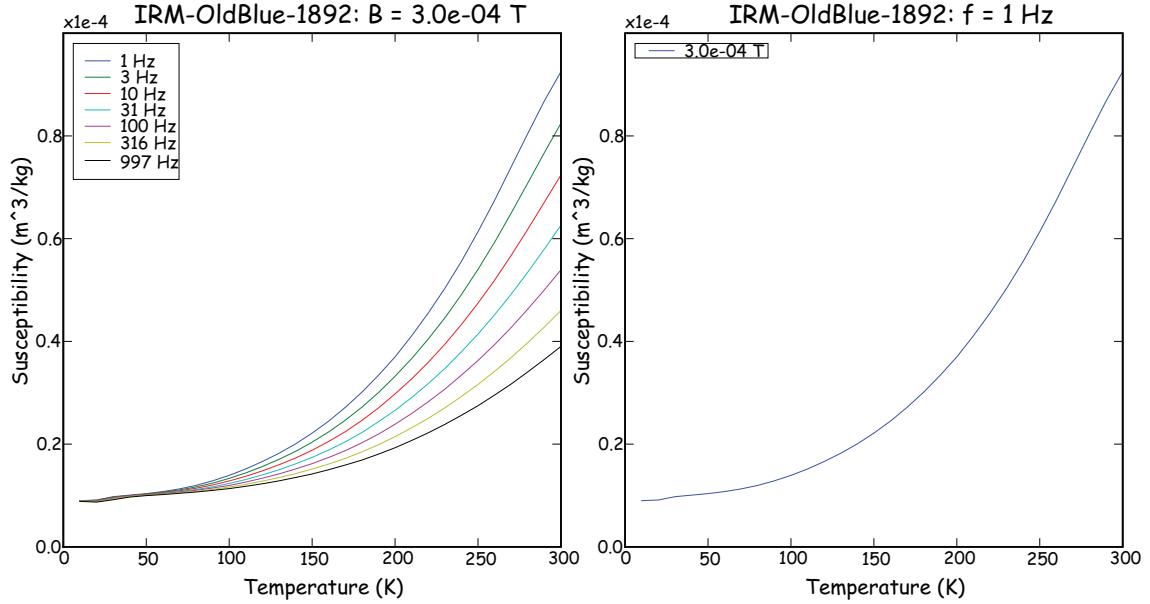
5.2.14 chi_magic.py

[Essentials Chapter 8] & [MagIC Database] [chi_magic docs]

It is sometimes useful to measure susceptibility as a function of temperature, applied field and frequency. Here we use a data set that came from the Tiva Canyon Tuff sequence (see Carter-Stiglitz, 2006). Use the program `chi_magic.py` to plot the data in the `magic_measurements` formatted file: `chi_magic_example.dat`.

```
$ chi_magic.py -f chi_magic_example.dat
IRM-Kappa-2352 1 out of  2
IRM-OldBlue-1892 2 out of  2
Skipping susceptibitily - AC field plot as a function of temperature
enter s[a]ve to save files,  [return] to quit
```

produced this plot:



You can see the dependence on temperature, frequency and applied field. These data support the suggestion that there is a strong superparamagnetic component in these specimens.

5.2.15 combine_magic.py

[MagIC Database] [combine_magic docs]

MagIC tables have many columns only some of which are used in a particular instance. So combining files of the same type must be done carefully to ensure that the right data come under the right headings. The program **combine_magic.py** can be used to combine any number of MagIC files from a given type. For an example of how to use this program, see AGM_magic.py.

5.2.16 common_mean.py

[Essentials Chapter 12] [common_mean docs]

Most paleomagnetists use some form of Fisher Statistics to decide if two directions are statistically distinct or not (see Essentials Chapter 11 for a discussion of those techniques. But often directional data are not fisher distributed and the parametric approach will give misleading answers. In these cases, one can use a bootstrap approach, described in detail in [Essentials Chapter 12]. Here we use the program **common_mean.py** for

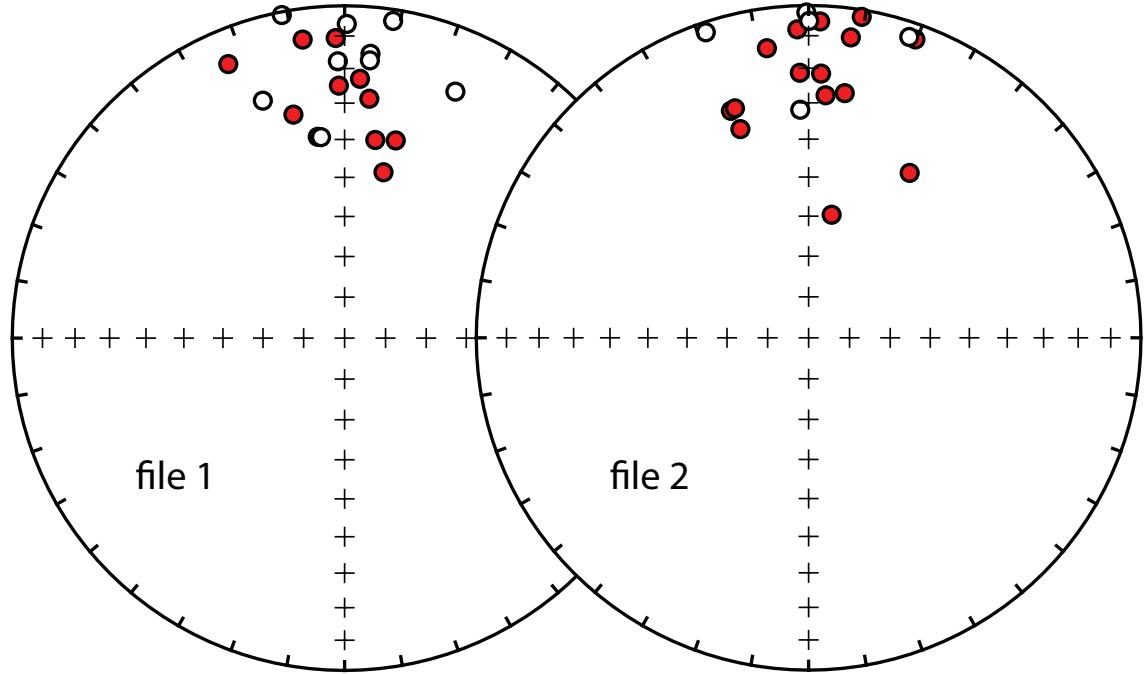
a bootstrap test for common mean to check whether two declination, inclination data sets have a common mean at the 95% level of confidence. The data sets are: *common_mean_ex_file1.dat* and *common_mean_ex_file2.dat*. But first, let's look at the data in equal area projection using the program *eqarea.py*.

The session:

```
$ eqarea.py -f common_mean_ex_file1.dat -sav
1 saved in common_mean_ex_file1.dat.svg

$ eqarea.py -f common_mean_ex_file2.dat -sav
1 saved in common_mean_ex_file2.dat.svg
```

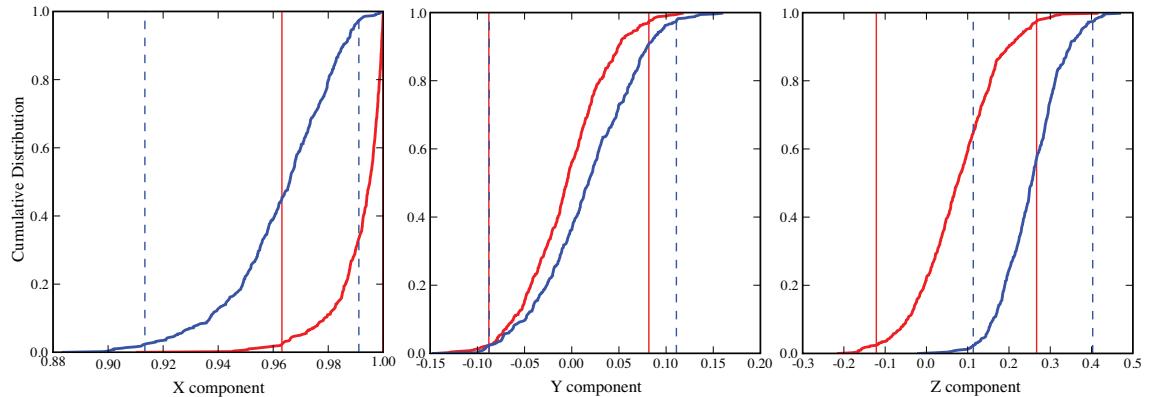
generates two .svg formatted files that look like these:



Now let's look at the common mean problem using **common_mean.py**.

```
$ common_mean.py -f common_mean_ex_file1.dat -f2 common_mean_ex_file2.dat
Doing first set of directions, please be patient..
Doing second set of directions, please be patient..
S[a]ve plots, <Return> to quit
```

The three plots are:

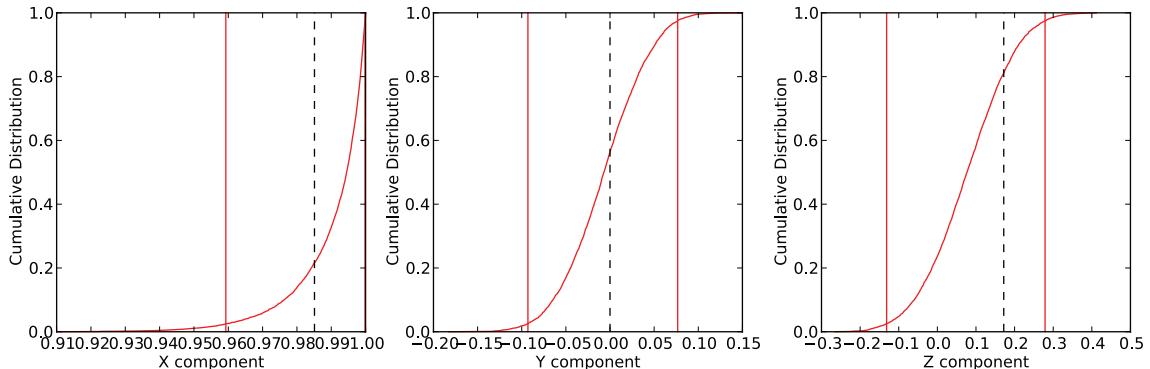


These suggest that the two data sets share a common mean.

Now compare the data in `common_mean_ex_file1.dat` with the expected direction at the 5°N latitude that these data were collected (Dec=0, Inc=9.9).

To do this, follow this transcript:

```
$ common_mean.py -f common_mean_ex_file1.dat -dir 0 9.9
Doing first set of directions, please be patient..
S[a]ve plots, <Return> to quit
```



Apparently the data (cumulative distribution functions) are entirely consistent with the expected direction (dashed lines are the cartesian coordinates of that).

5.2.17 cont_rot.py

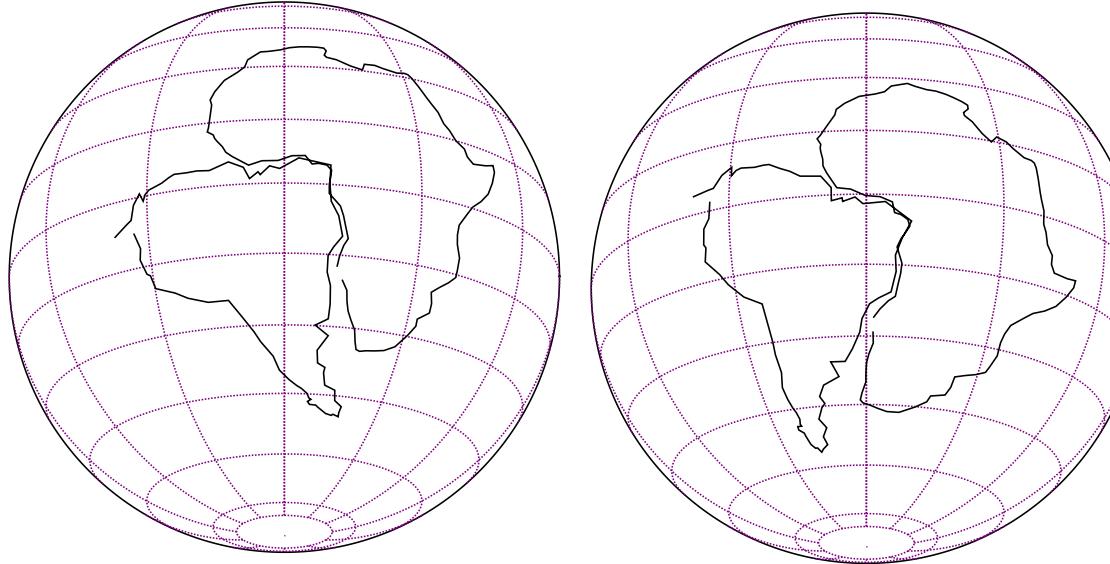
[Essentials Chapter 16 and Essentials Appendix A.3.5.] [cont_rot docs]

Use the program `cont_rot.py` to make an orthographic projection with latitude = -20° and longitude = 0° at the center of the African and South American continents reconstructed to 180 Ma using the Torsvik et al. (2008)

poles of finite rotation. Do this by first holding Africa fixed. Move the output plot to *fixed_africa.svg*. Then make the plot for Africa adjusted to the paleomagnetic reference frame. Make the continental outlines in black lines and set the resolution to 'low'.

```
$ cont_rot.py -con af:sam -prj ortho -eye -20 0 -sym k- 1 -age 180 -res l
S[a]ve to save plot, Return to quit: a
1 saved in Cont_rot.pdf
$ mv Cont_rot.pdf fixed_africa.pdf
$ cont_rot.py -con af:sam -prj ortho -eye -20 0 -sym k- 1 -age 180 \
-res l -sac
S[a]ve to save plot, Return to quit: a
1 saved in Cont_rot.pdf
```

These commands generated the following plots (first on left, second on right):



5.2.18 convert2unix.py

[convert2unix docs]

This is a handy little script that turns Windows or Mac file formatted files (not Word or other proprietary formats) into Unix file format. It does the change in place, overwriting the original file.

5.2.19 convert_samples.py

[MagIC Database] [convert_samples docs]

If one of the MagIC related programs in PmagPy created a very lean looking *er_samples.txt* file (for example using *azdip_magic.py*) and you need to add more information (say, latitude, longitude, lithology, etc.), you can convert the *er_samples.txt* file into an *orient.txt* file format, edit it in, for example Excel, and then re-import it back into the *er_samples.txt* file format. Try this on the *er_samples* formatted file in the *convert_samples* directory, *convert_samples_example.dat*.

```
$ convert_samples.py -f convert_samples_example.dat
Data saved in: orient_Northern_Iceland.txt
```

5.2.20 core_depthplot.py

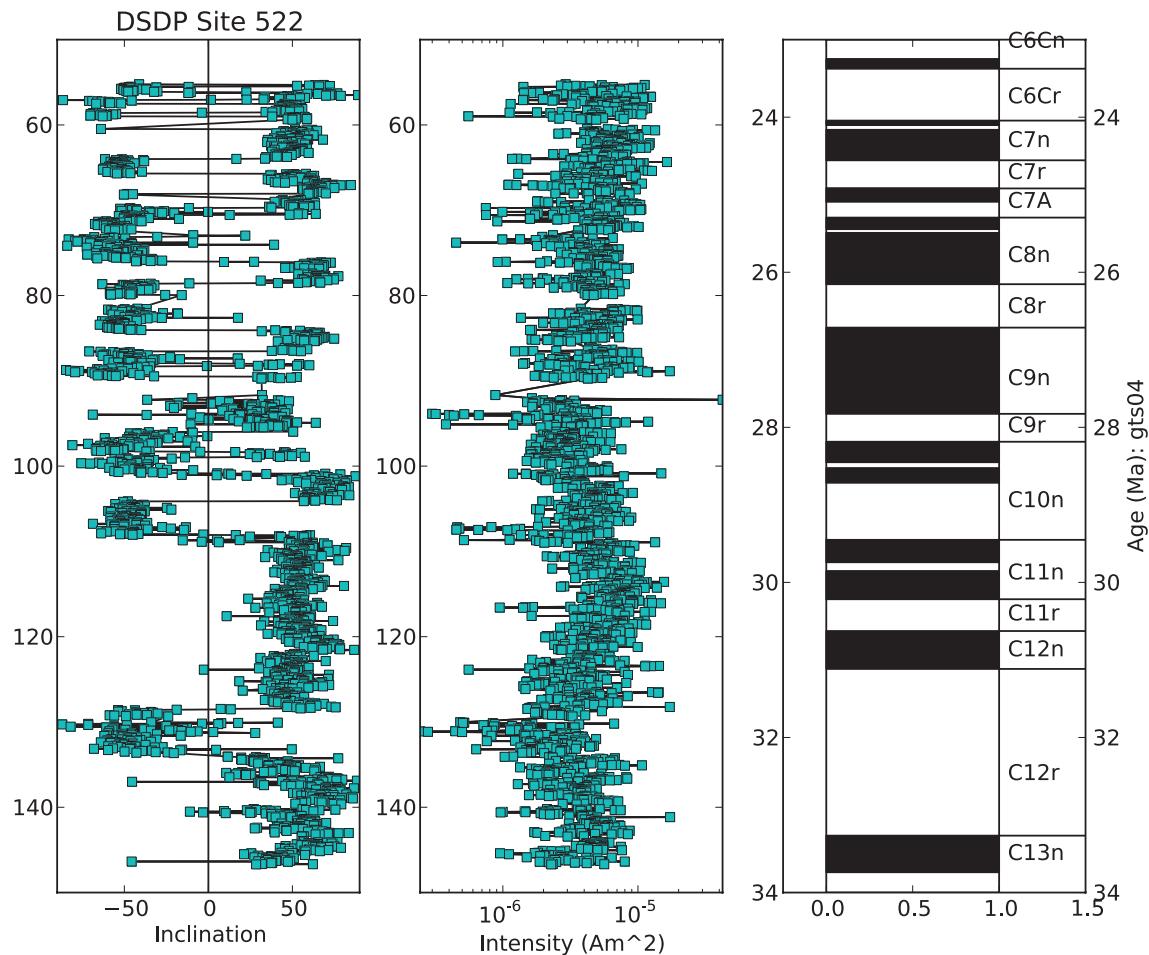
[[Essentials Chapter 15] [core_depthplot docs]

Use the program **core_depthplot.py** to plot various measurement data versus sample depth. The data must be in the MagIC data formats. The program will plot whole core data, discrete sample at a bulk demagnetization step, data from vector demagnetization experiments, and so on. There are many options, so check the help menu before you begin.

We can try this out on some data from DSDP Hole 522, measured by Tauxe and Hartl (1997). These can be downloaded and unpacked (see *download_magic.py* for details), or you can try it out on the data files in the directory **core_depthplot**. You must specify a lab-protocol (LP) for plotting. In this example, we will plot the alternating field (AF) data after the 15 mT step. The magnetizations will be plotted on a log scale and, as this is a record of the Oligocene, we will plot the Oligocene time scale, using the calibration of Gradstein et al. (2004), commonly referred to as “GTS04” for the the Oligocene. We are only interested in the data between 50 and 150 meters (the -d option sets this) and we will suppress the declinations (-D).

```
$ core_depthplot.py -fsa er_samples.txt -LP AF 15 -log -d 50 150 -ts gts04 23 34 -D
```

will produce the plot:



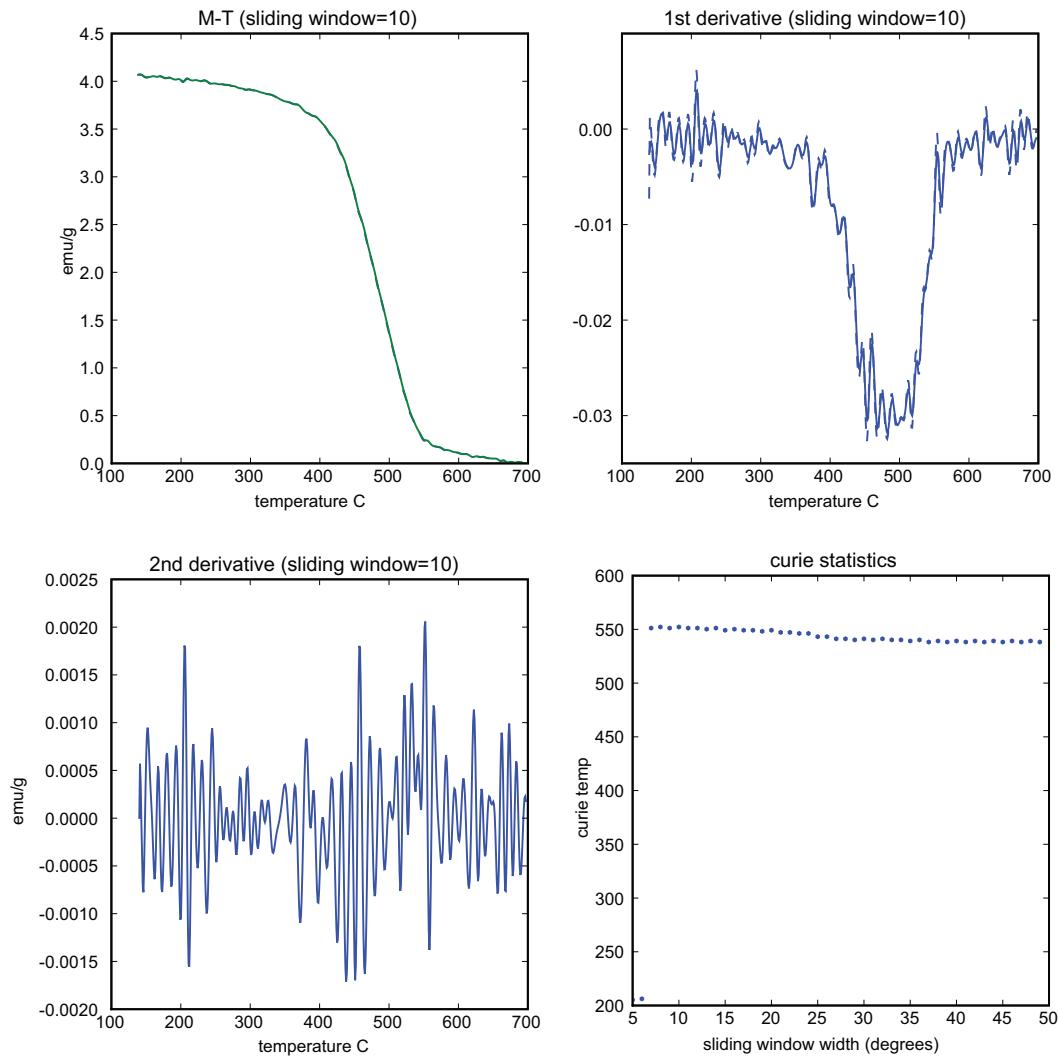
5.2.21 curie.py

[Essentials Chapter 6] [curie docs]

Use the program **curie.py** to interpret Curie temperature data in the example file *curie_example.dat*. Use a smoothing window of 10° .

```
%curie.py -f curie_example.dat -w 10
second derivative maximum is at T=552
```

which generates these plots:



5.2.22 customize_criteria.py

[MagIC Database] [customize_criteria docs]

NB: The best place to customize your selection criteria is within Demag GUI or Thellier GUI. But if you want to do it on the command line, then here's how.

The MagIC database allows documentation of which criteria were used in selecting data on a specimen, sample or site level and to easily apply those criteria (and re-apply them as they change) in preparing the different

tables. These choices are stored in the *pmag_criteria* table in each MagIC project directory (see Pmag GUI documentation).

Certain **PmagPy** programs use the datafile *pmag_criteria.txt* to select data (for example **thellier_magic.py** and **specimens_results_magic.py**). To customize these criteria for your own data sets, you can use the program **customize_criteria.py**. This program is also called by the **Pmag GUI** under the Utilities menu. Try it out on *pmag_criteria.txt*. This is a “full vector” set of criteria - meaning that it has both directions and intensity flags set. Change the *specimen_alpha95* cutoff to 180. from whatever it is now set to. Save the output to a new file named *new_criteria.txt*.

```
$ customize_criteria.py -f pmag_criteria.txt -F new_criteria.txt
Acceptance criteria read in from pmag_criteria.txt
[0] Use no acceptance criteria?
[1] Use default criteria
[2] customize criteria
2
Enter new threshold value.
Return to keep default.
Leave blank to not use as a criterion

sample_alpha95 10
new value: 5
sample_int_n 2
new value: 2
sample_int_sigma 5e-6
new value:
sample_int_sigma_perc 15
new value:
.....
Criteria saved in pmag_criteria.txt

Pmag Criteria stored in pmag_criteria.txt
```

Note that the default place for the PmagPy programs to look for criteria is in *pmag_criteria.txt*, so you should probably rename the new one that for it to take effect as your new default.

5.2.23 dayplot_magic.py

[Essentials Chapter 5] [dayplot_magic docs]

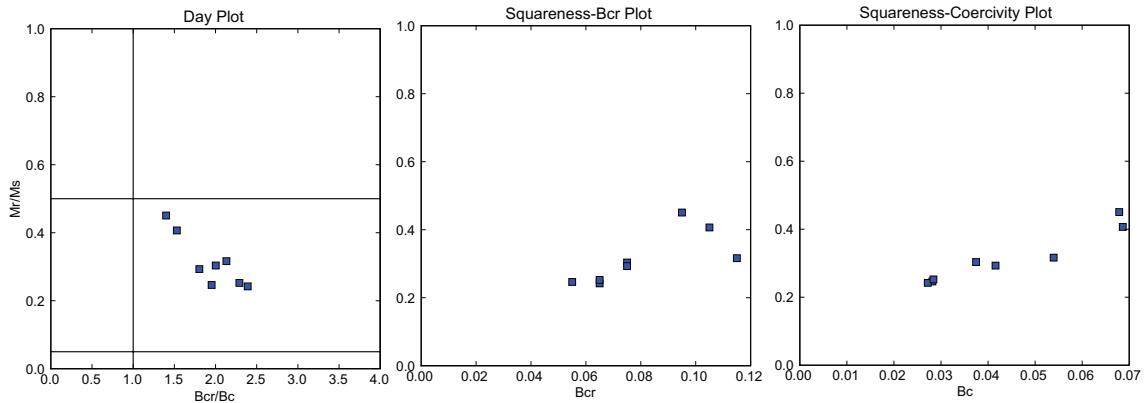
Use the program **dayplot_magic.py** to make Day (Day et al., 1977), or Squareness-Coercivity and Squareness-Coercivity of Remanence plots (e.g., Tauxe et al., 2002) from the rmag_hyseresis formatted data in *dayplot_magic_example.dat*.

The session:

```
$ dayplot_magic.py -f dayplot_magic_example.dat
```

```
S[a]ve to save plots, return to quit:
```

gives the plots:



5.2.24 demag_gui.py

[Essentials Chapter 7] [demag_gui docs]

The program **demag_gui.py** is used by Pmag GUI for interpreting demagnetization experimental data. See Demag GUI for guidance.

5.2.25 di_eq.py

[Essentials Appendix B] [di_eq docs]

Paleomagnetic data are frequently plotted in equal area projection. PmagPy has several plotting programs which do this (e.g., eqarea.py, but occasionally it is handy to be able to convert the directions to X,Y coordinates directly, without plotting them at all. The program **di_eq.py** does this. Here is an example transcript of a session using the datafile *di_eq_example.dat*:

```
$ di_eq.py -f di_eq_example.dat
-0.239410 -0.893491
0.436413 0.712161
0.063844 0.760300
0.321447 0.686216
0.322720 0.670562
0.407412 0.540654
.
.
.
```

5.2.26 di_geo.py

[Essentials Chapter 9] and Changing coordinate systems [di_geo docs]

Use the programs **di_geo.py** to convert $D = 8.1, I = 45.2$ from specimen coordinates to geographic adjusted coordinates. The orientation of laboratory arrow on the specimen was: azimuth = 347; plunge = 27. **di_geo.py** works in the usual three ways (interactive data entry, command line file specification or from standard input). So for a quickie answer for a single specimen, you can use the interactive mode:

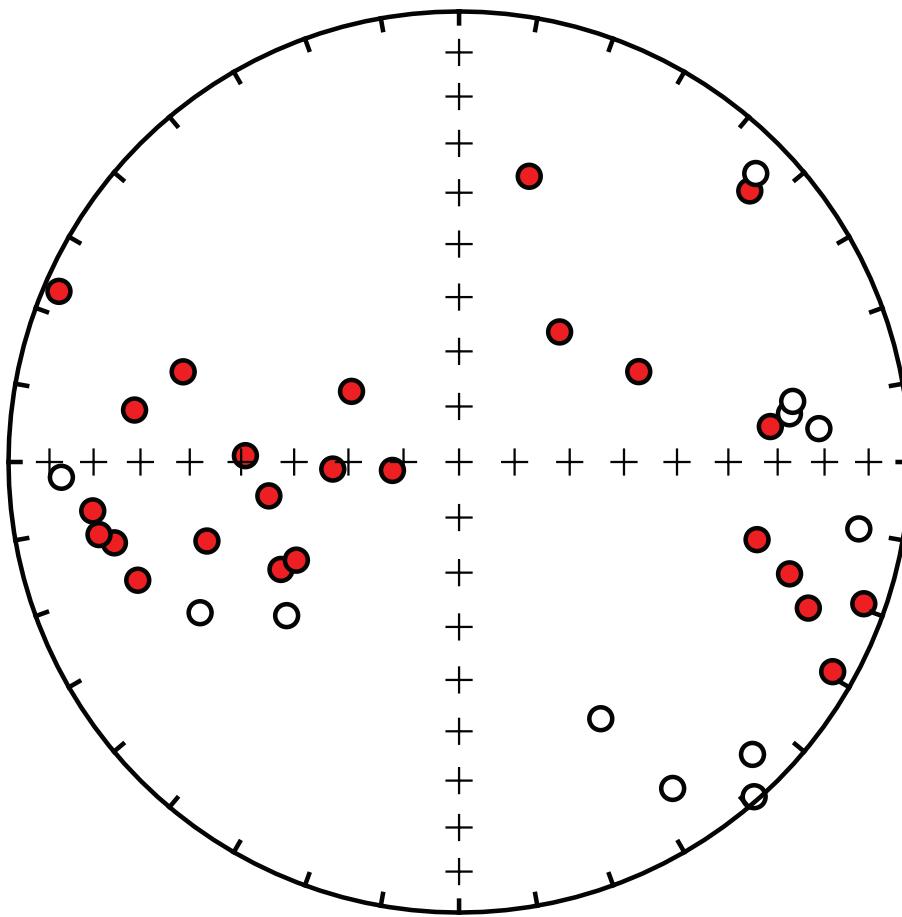
```
$ di_geo.py -i
Declination: <cntrl-D> to quit 81
Inclination: 45.2
Azimuth: 347
Plunge: 27
94.8    43.0
```

which spits out our answer of Declination = 5.3 and inclination = 71.6.

For more data, it is handy to use the file entry options. There are a bunch of declination, inclination, azimuth and plunge data in the file *di_geo-example.dat* in the *di_geo* directory. First look at the data in specimen coordinates in equal area projection, using the program *eqarea.py*. Note that this program only pays attention to the first two columns so it will ignore the orientation information.

```
$ eqarea.py -f di_geo_example.dat
```

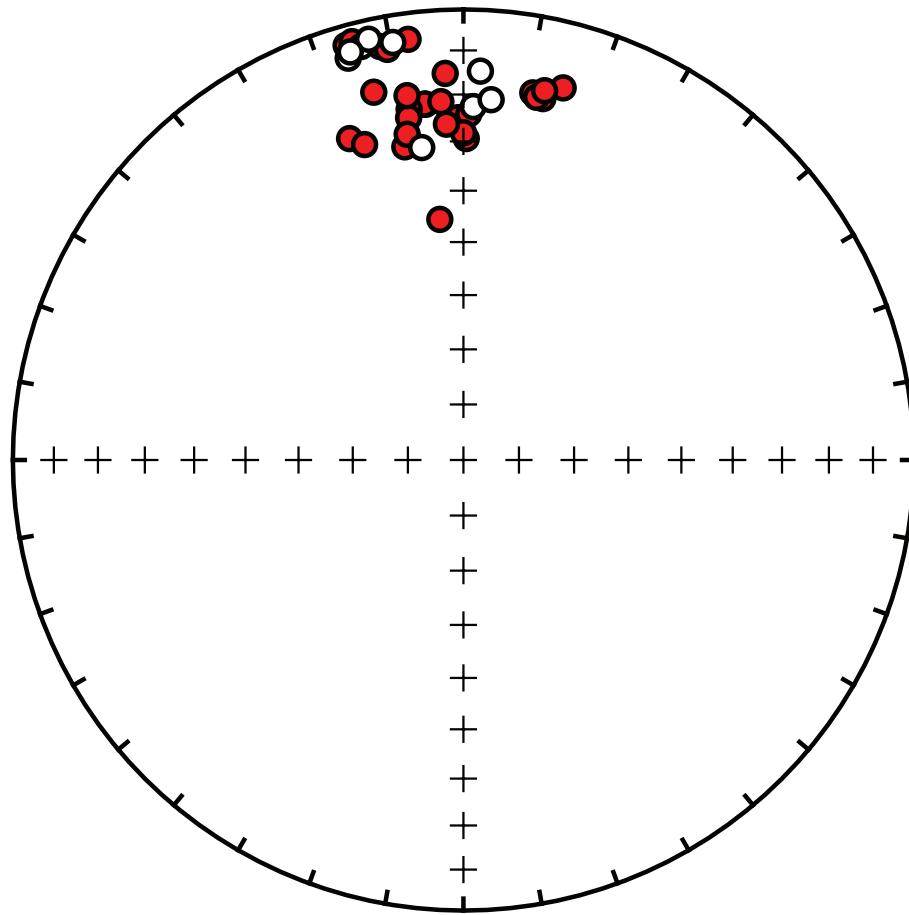
which should look like this:



The data are highly scattered and we hope that the geographic coordinate system looks better! To find out try:

```
di_geo.py -f di_geo_example.dat >di_geo.out; eqarea.py -f di_geo.out
```

which looks like this:



These data are clearly much better grouped.

5.2.27 di_rot.py

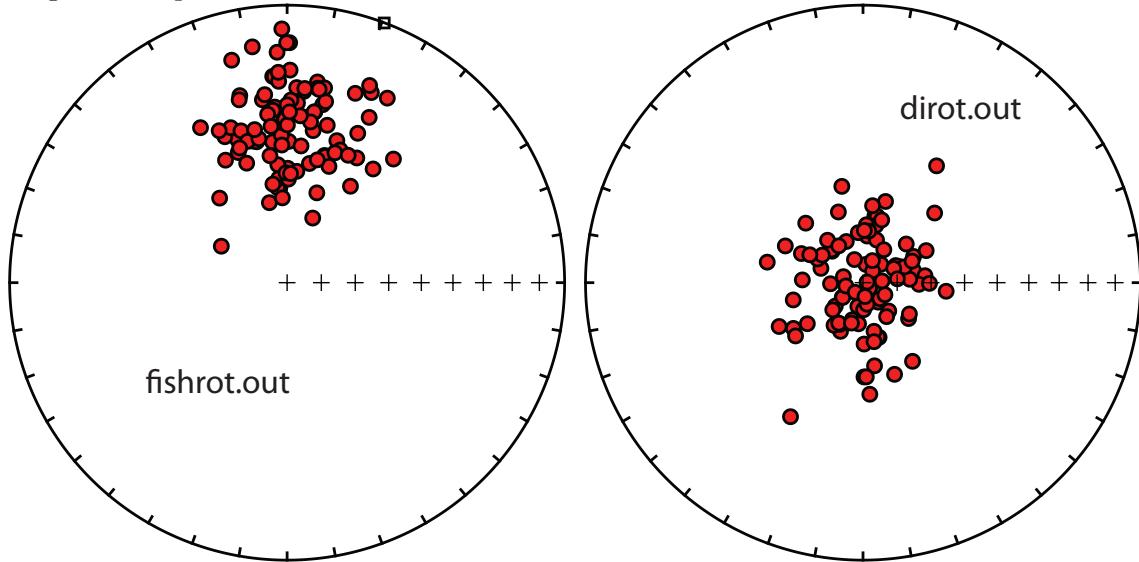
[Essentials Chapter 11] [di_rot docs]

Generate a Fisher distributed set of data from a population with a mean direction of $D = 0, I = 42$ using the program **fishrot.py**. Calculate the mean direction of the data set using **gofish.py**. Now use the program **di_rot.py** to rotate the set of directions to the mean direction. Look at the data before and after rotation using **eqarea.py**.

```
$ fishrot.py -I 42 >fishrot.out
$ gofish.py <fishrot.out
      1.7    42.4    100   95.3720    21.4     3.1
$ di_rot.py -f fishrot.out -F dirot.out -D 1.7 -I 42.4
```

```
$ eqarea.py -f fishrot.out
$ eqarea.py -f dirot.out
```

which generates plots like these:



Note that every instance of **fisher.py** will draw a different sample from a Fisher distribution and your exact plot and average values will be different in detail every time you try this (and that's part of the fun of statistical simulation.)

5.2.28 di_tilt.py

[Essentials Chapter 9] and Changing coordinate systems [di_tilt docs]

Use the program **di_tilt.py** to rotate a direction of Declination = 5.3 and Inclination = 71.6 to “stratigraphic” coordinates. The strike was 135 and the dip was 21. The convention in this program is to use the dip direction, which is to the “right” of this strike.

Here is a session with **di_tilt.py** using the interactive option:

```
$ di_tilt.py -i
Declination: <cntl-D> to quit 5.3
Inclination: 71.6
Dip direction: 225
Dip: 21
      285.7    76.6
Declination: <cntl-D> to quit ^D
```

Good-bye

Try the same on the data file saved as *di_tilt_example.dat* using the command line -f switch:

5.2.29 di_vgp.py

[Essentials Chapter 2] [di_vgp docs]

Use the program **di_vgp** to convert the following:

<i>D</i>	<i>I</i>	λ_s (N)	ϕ_s (E)
11	63	55	13
154	-58	45.5	-73

Here is a transcript of a typical session using the command line option for file name entry:

```
$ di_vgp.py -f di_vgp_example.dat
154.7    77.3
       6.6   -69.6
```

5.2.30 dipole_pinc.py

[Essentials Chapter 2] [dipole_pinc docs]

Calculate the expected inclination at a paleolatitude of 24°S.

```
$ dipole_pinc.py -i
Paleolat for converting to inclination: <cntl-D> to quit -24
      -41.7
Paleolat for converting to inclination: <cntl-D> to quit ^D
Good-bye
```

5.2.31 dipole_plat.py

[Essentials Chapter 2] [dipole_plat docs]

Calculate the paleolatitude for an average inclination of 23°.

```
$ dipole_plat.py -i
Inclination for converting to paleolatitude: <cntl-D> to quit 23
      12.0
Inclination for converting to paleolatitude: <cntl-D> to quit ^D
Good-bye
```

5.2.32 dir_cart.py

[Essentials Chapter 2] [dir_cart docs]

Use the program **dir_cart.py** to convert the following data from declination D , inclination I and intensity M to x_1, x_2, x_3 .

D	I	M (μAm^2)
20	46	1.3
175	-24	4.2

You can enter D, I, M data into data file, then running the program by typing what is after the prompts (%) [the other stuff is computer responses]:

```
$ cat > dir_cart_example.dat
20 46 1.3
175 -24 4.2
^D
$ dir_cart.py <dir_cart_example.dat
8.4859e-01 3.0886e-01 9.3514e-01
-3.8223e+00 3.3441e-01 -1.7083e+00
```

Or you could use **dir_cart.py** interactively as in:

```
$ dir_cart.py -i
```

```
Declination: [cntrl-D to quit]
Good-bye
```

```
$ dir_cart.py -i
Declination: [cntrl-D to quit] 20
Inclination: 46
Intensity [return for unity]: 1.3
8.4859e-01 3.0886e-01 9.3514e-01
Declination: [cntrl-D to quit] 175
Inclination: -24
Intensity [return for unity]: 4.2
-3.8223e+00 3.3441e-01 -1.7083e+00
Declination: [cntrl-D to quit] ^D
Good-bye
```

5.2.33 dmag_magic.py

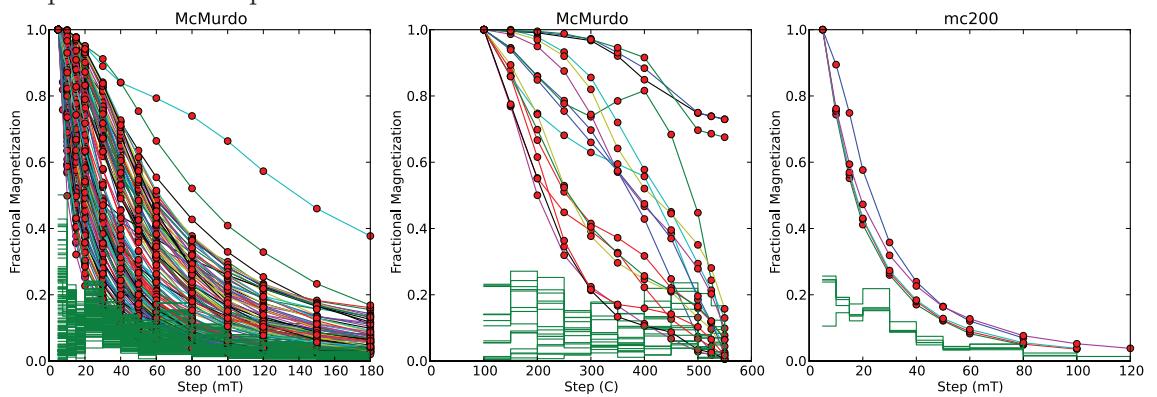
[Essentials Chapter 9] and [MagIC Database] [dmag_magic docs]

Use **dmag_magic.py** to plot out the decay of all alternating field demagnetization experiments in the `magic_measurements` formatted file in `dmag_magic_example.dat`. These are from Lawrence et al. (2009). Repeat for all thermal measurements, but exclude all the data acquired during the thermal but not paleointensity experiments. Try this at the location level and then at the site level.

Here is a transcript of a session:

```
$ dmag_magic.py -f dmag_magic_example.dat -LT AF
5921 records read from dmag_magic_example.dat
McMurdo plotting by: er_location_name
S[a]ve to save plot, [q]uit, Return to continue: a
1 saved in McMurdo_LT-AF-Z.svg
$ dmag_magic.py -f dmag_magic_example.dat -LT T -XLP PI
5921 records read from dmag_magic_example.dat
McMurdo plotting by: er_location_name
S[a]ve to save plot, [q]uit, Return to continue: a
1 saved in McMurdo_LT-T-Z.svg
$ dmag_magic.py -f dmag_magic_example.dat -LT AF -obj sit
5921 records read from dmag_magic_example.dat
mc20 plotting by: er_site_name
S[a]ve to save plot, [q]uit, Return to continue:
mc200 plotting by: er_site_name
S[a]ve to save plot, [q]uit, Return to continue: a
1 saved in mc200_LT-AF-Z.svg
```

which produced these plots:



5.2.34 download_magic.py

[MagIC] [download_magic docs]

This program unpacks .txt files downloaded from the MagIC database into individual directories for each location into which the individual files for each table (e.g., *er_locations.txt*, *magic_measurements.txt*, *pmag_results.txt* and so on) get placed. As an example, go to the MagIC data base at <http://earthref.org/MAGIC/search>. Enter “Tauxe and 2004” into the Reference Text Search field will show you several references. Look for the one for Tauxe, L., Luskin, C., Selkin, P., Gans, P. and Calvert, A. (2004). Download the text file under the “Data” column and save it to your desktop. Make a folder into which you should put the downloaded txt file called MagIC_download and move the file into it. Now use the program **download_magic.py** to unpack the .txt file (*zmab0083201tmp03.txt*).

```
$ cd MagIC_download
$ download_magic.py -f zmab0083201tmp03.txt
working on: 'er_locations'
er_locations data put in ./er_locations.txt
working on: 'er_sites'
er_sites data put in ./er_sites.txt
working on: 'er_samples'
er_samples data put in ./er_samples.txt
working on: 'er_specimens'

.
.
.

location_1: Snake River
unpacking: ./er_locations.txt
1 read in
1 stored in ./Location_1/er_locations.txt
unpacking: ./er_sites.txt
27 read in
27 stored in ./Location_1/er_sites.txt
unpacking: ./er_samples.txt
271 read in
271 stored in ./Location_1/er_samples.txt
unpacking: ./er_specimens.txt

.
```

You can change directories into each Location directory (in this case only one) and examine the data using the **PmagPy** GUI programs (e.g., pmag.gui.py).

5.2.35 eigs_s.py

[Essentials Chapter 13] [eigs_s docs]

Print out the eigenparameters in the file *eigs_s_example.dat* and then convert them to tensor data in the .s format (x11,x22,x33,x12,x13,x23).

This session uses the unix utility **cat** to print the data. [You could use the Ms-Dos form **type** in a Windows command line window.] Then, it prints the tensor data to the screen.

```
$ cat eigs_s_example.dat
0.33127 239.53 44.70 0.33351 126.62 21.47 0.33521 19.03 37.54
0.33177 281.12 6.18 0.33218 169.79 73.43 0.33603 12.82 15.32
...
$ eigs_s.py -f eigs_s_example.dat
0.33416328 0.33280227 0.33303446 -0.00016631 0.00123163 0.00135521
0.33555713 0.33197427 0.33246869 0.00085685 0.00025266 0.00098151
0.33585301 0.33140355 0.33274350 0.00132308 0.00117787 0.00000455
...
```

5.2.36 eq_di.py

[Essentials Appendix B] [eq_di docs]

Data are frequently published as equal area projections and not listed in data tables. These data can be digitized as x,y data (assuming the outer rim is unity) and converted to approximate directions with the program **eq_di.py**. To use this program, install a graph digitizer (GraphClick from <http://www.arizona-software.ch/graphclick/> works on Macs).

Digitize the data from the equal area projection saved in the file *eqarea.png* in the *eq_di* directory. You should only work on one hemisphere at a time (upper or lower) and save each hemisphere in its own file. Then you can convert the X,Y data to approximate dec and inc data - the quality of the data depends on your care in digitizing and the quality of the figure that you are digitizing.

Try out **eq_di.py** on your datafile, or use *eq_di-example.dat* which are the digitized data from the lower hemisphere and check your work with **eqarea.py**. You should retrieve the lower hemisphere points from the **eqarea.py** example.

```
$ eq_di.py -f eq_di_example.dat >tmp  
$ eqarea.py -f tmp
```

NB: To indicate that your data are UPPER hemisphere (negative inclinations), use the `-up` switch.

You can verify the process by comparing the plot generated for these data using `eqarea.py` with the original `.png` file.

5.2.37 eqarea.py

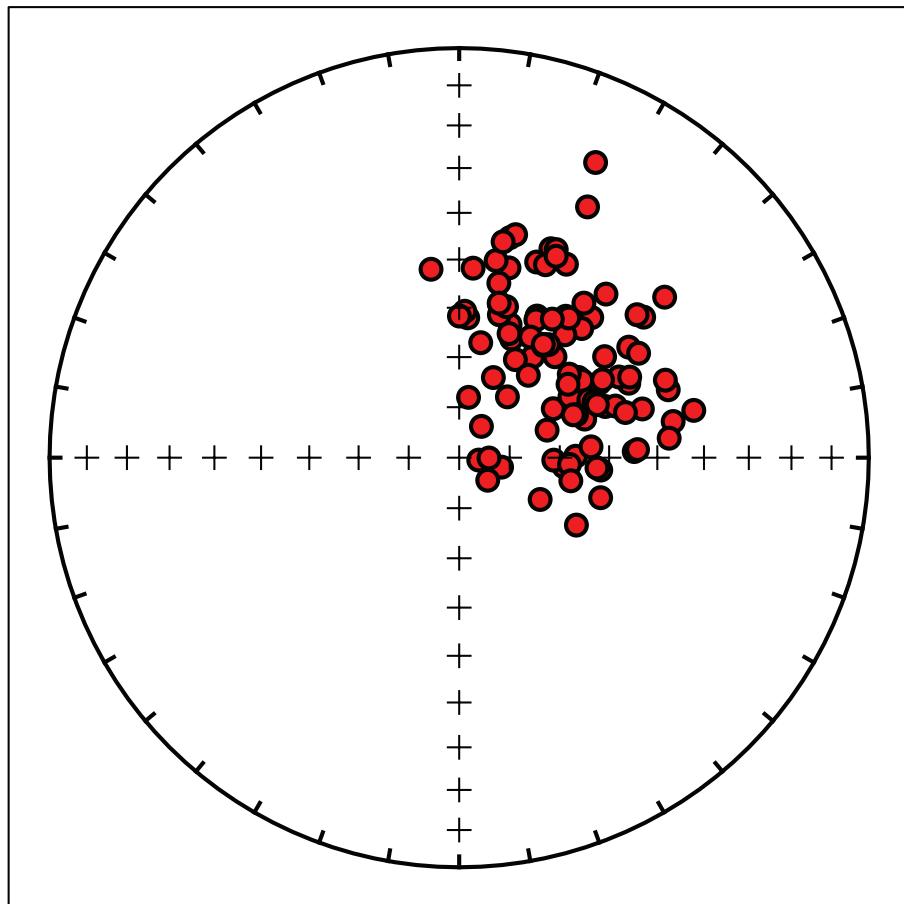
[Essentials Chapter 2] and [Essentials Appendix B.1] [eqarea docs]

Use the program `fishrot.py` to generate a Fisher distributed set of data drawn from a distribution with mean declination of 42° and a mean inclination of 60° . Save this to a file called `fishrot.out`. Use `eqarea.py` to plot an equal area projection of the data.

```
$ fishrot.py -D 42 -I 60 > fishrot.out  
$ eqarea.py -f fishrot.out
```

which produces the plot:

Equal Area Plot



5.2.38 eqarea_ell.py

[Essentials Chapters 11] and [Essentials Chapter 12] [eqarea_ell docs]

Use the program `tk03.py` to generate a set of simulated data for a latitude of 42°N including reversals. Then use the program `eqarea_ell.py` to plot an equal area projection of the directions in `di_example.txt` and plot confidence ellipses. Here is an example for Bingham ellipses.

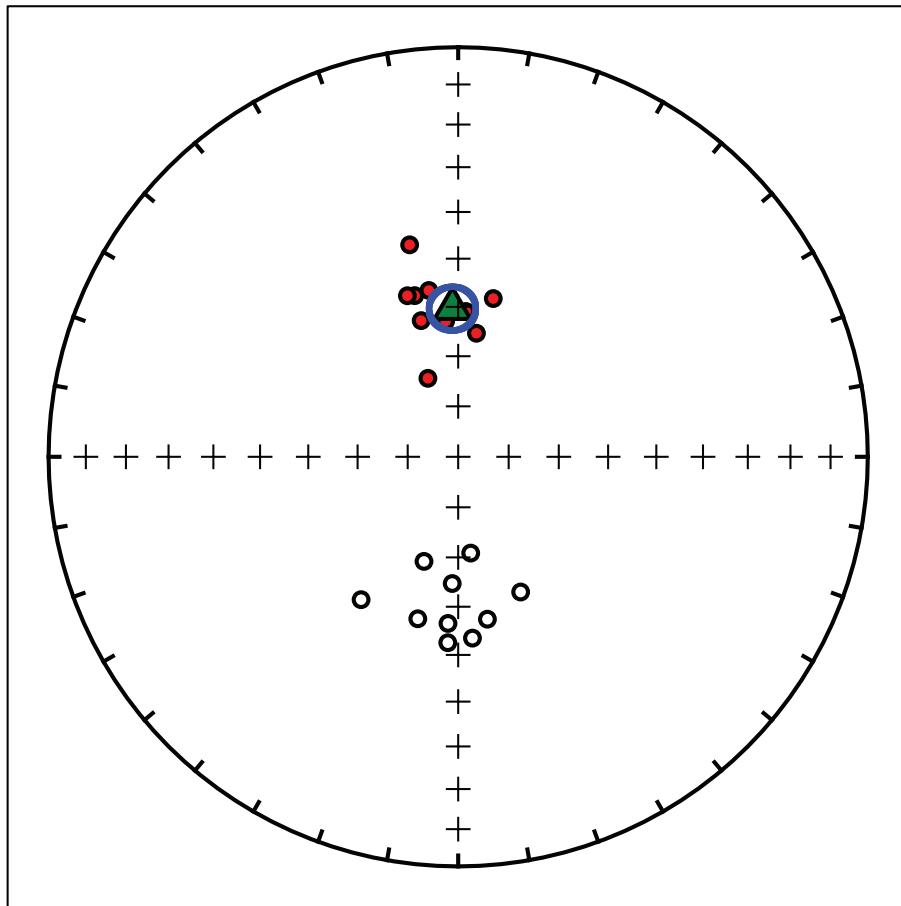
```
$ tk03.py -lat 42 -rev >tk03.out
$ eqarea_ell.py -f tk03.out -ell B
      Zdec    21.0
      Edec   105.7
```

```
Eta      4.5
n        20
Einc    10.0
Zinc   -27.6
Zeta     4.5
dec    357.8
inc    60.3
S[a]ve to save plot, [q]uit, Return to continue: a
1 saved in tk03.out_eq.svg
```

which produces a plot like this:

Bingham confidence ellipse

tk03.out



Other ellipses are Kent, Fisher and bootstrapped ellipses. Check the documentation for details.

5.2.39 eqarea_magic.py

[MagIC Database] [eqarea_magic docs]

Follow the instructions for downloading and unpacking a data file from the MagIC database or use the file in the *download_magic* directory already

downloaded from the MagIC website. Plot the directional data for the study from the *pmag_results.txt* file along with the bootstrapped confidence ellipse.

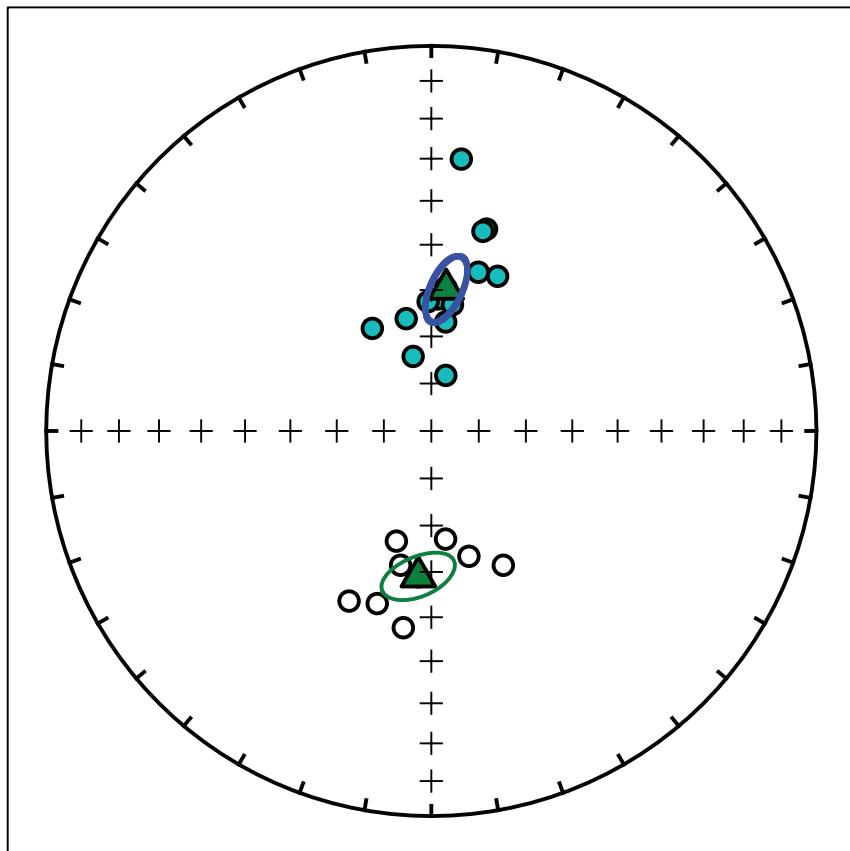
```
$ eqarea_magic.py -obj loc -crd g -f pmag_results.txt -ell Be
24 records read from ./pmag_results.txt
All
sr01 GM-ARAR-AP:LP-DC5:LP-DIR-AF:LP-DIR-T:LP-PI-ALT-PTRM:LP-PI-TRM-ZI    330.1    64.9
sr03 GM-ARAR-AP:LP-DC5:LP-DIR-AF:LP-DIR-T    151.8   -57.5
sr04 GM-ARAR-AP:LP-DC5:LP-DIR-AF:LP-DIR-T    16.5    54.6
.
.
.
sr31 GM-ARAR-AP:LP-DC5:LP-DIR-AF:LP-DIR-T    23.2    54.0
sr34 GM-ARAR-AP:LP-DC5:LP-DIR-AF:LP-DIR-T:LP-PI-ALT-PTRM:LP-PI-TRM-ZI    205.8   -49.4
sr36 GM-ARAR-AP:LP-DC5:LP-DIR-AF:LP-DIR-T    197.6   -65.5
sr39 GM-ARAR-AP:LP-DC5:LP-DIR-AF:LP-DIR-T:LP-PI-ALT-PTRM:LP-PI-TRM-ZI    188.1   -47.2
sr40 GM-ARAR-AP:LP-DC5:LP-DIR-AF:LP-DIR-T    192.9   -60.7
Normal Pole GM-ARAR-AP:LP-DC5:LP-DIR-AF:LP-DIR-T    6.1    59.6
Reverse pole GM-ARAR-AP:LP-DC5:LP-DIR-AF:LP-DIR-T    185.1   -58.8
Grand Mean pole GM-ARAR-AP:LP-DC5:LP-DIR-AF:LP-DIR-T    5.7    59.3
mode 1
    Zdec    111.1
    Edec    206.0
    Eta     7.8
    n       1
    Einc    28.9
    Zinc    8.7
    Zeta    3.3
    dec     6.0
    inc     59.6
mode 2
    Zdec    248.0
    Edec    150.1
    Eta     4.3
    n       1
    Einc    26.4
    Zinc    15.4
    Zeta    8.0
    dec     185.1
    inc    -58.8
```

```
S[a]ve to save plot, [q]uit, Return to continue: a
1 saved in LO:_Snake_River_SI:__SA:__SP:__CO:_gu_TY:_eqarea_.svg
```

makes this plot:

Bootstrapped confidence ellipse

All



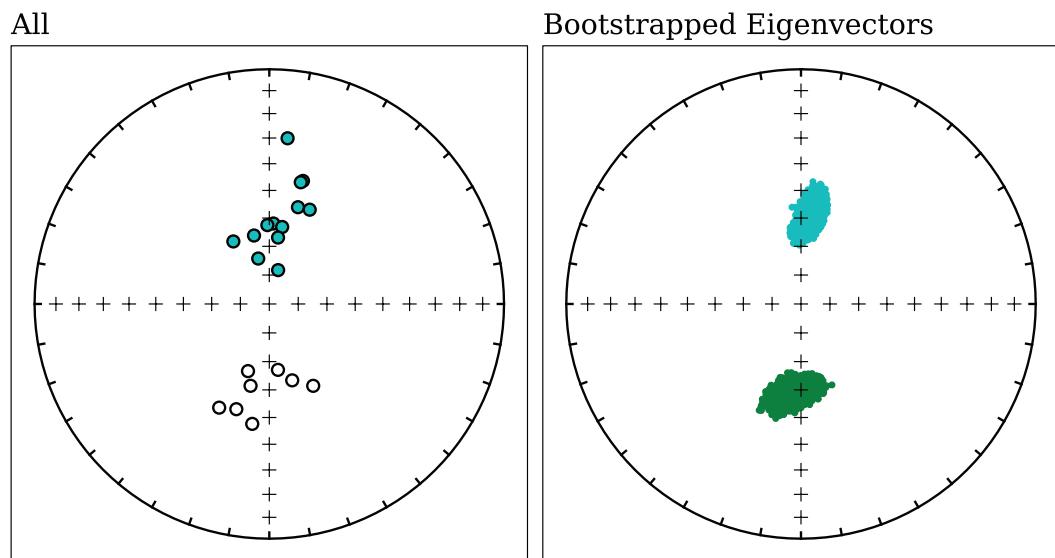
The information printed to the window is the pmag_result_name in the data table, the method codes (here the geochronology method, the type of demagnetization code and the types of demagnetization experiments), and each site mean declination inclination. The information following “mode 1” are the bootstrapped ellipse parameters.

Some data are study averages and some are individual sites.

Use `magic_select.py` to select only the individual site data. Try the

```
$ magic_select.py -f pmag_results.txt -key data_type i 'T' -F site_results.txt
$ eqarea_magic.py -f site_results.txt -ell Bv
21 records read from ./site_results.txt
All
sr01 GM-ARAR-AP:LP-DC5:LP-DIR-AF:LP-DIR-T:LP-PI-ALT-PTRM:LP-PI-TRM-ZI    330.1    64.9
sr03 GM-ARAR-AP:LP-DC5:LP-DIR-AF:LP-DIR-T    151.8   -57.5
sr04 GM-ARAR-AP:LP-DC5:LP-DIR-AF:LP-DIR-T    16.5    54.6
sr09 GM-ARAR-AP:LP-DC5:LP-DIR-AF:LP-DIR-T    14.6    77.9
.
.
.
sr36 GM-ARAR-AP:LP-DC5:LP-DIR-AF:LP-DIR-T    197.6   -65.5
sr39 GM-ARAR-AP:LP-DC5:LP-DIR-AF:LP-DIR-T:LP-PI-ALT-PTRM:LP-PI-TRM-ZI    188.1   -47.2
sr40 GM-ARAR-AP:LP-DC5:LP-DIR-AF:LP-DIR-T    192.9   -60.7
S[a]ve to save plot, [q]uit, Return to continue: a
1 saved in LO:_Snake_River_SI:__SA:__SP:__CO:g_TY:_eqarea_.svg
2 saved in LO:_Snake_River_SI:__SA:__SP:__CO:g_TY:_bdirs_.svg
```

which produces plots like:



5.2.40 find_EI.py

[Essentials Chapter 14][find_EI docs]

A data file was prepared using tk03.py to simulate directions at a latitude of 42°. Use the program dipole_pinc.py to find what the expected inclination at this latitude is!

```
$ dipole_pinc.py -i
Paleolat for converting to inclination: <cntl-D> to quit 42
61.0
^D
Paleolat for converting to inclination: <cntl-D> to quit ^D
Good-bye
```

The data were “flattened” with the program squish.py which uses the formula $\tan I_o = f \tan I_f$ to simulate inclination error and saved in a data file *find_EI_example.dat* in the *find_EI* directory.

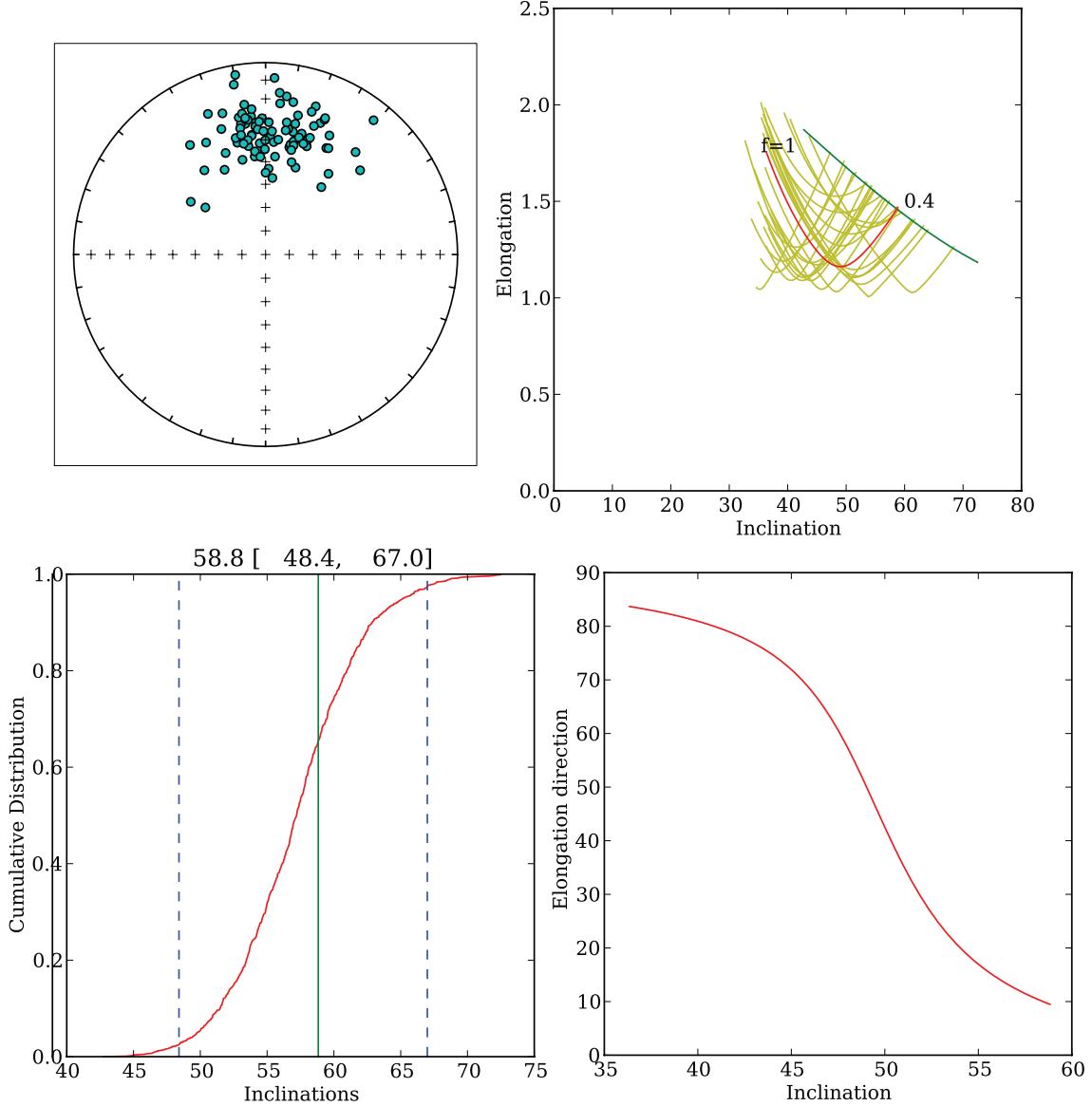
```
$ tk03.py -lat 42 > tk03.out
$ squish.py -flt .4 -f tk03.out -F find_EI_example.dat
```

Use the program **find_EI.py** to find the optimum flattening factor f which, when used to “unflatten” the data yields inclination and elongation (ratio of major and minor eigenvalues of orientation matrix, see the section on eigenvalues in the textbook) most consistent with the TK03.GAD paleosecular variation model of Tauxe and Kent (2004).

```
$ find_EI.py -f find_EI_example.dat
Bootstrapping.... be patient
25  out of  1000
50  out of  1000
75  out of  1000
100 out of  1000
.
.
.
Io Inc  I_lower, I_upper, Elon, E_lower, E_upper
38.9  =>    58.8 _   48.4 ^   67.0:  1.4679 _ 1.2912 ^ 1.7337
S[a]ve plots - <return> to quit:  a
2 saved in  findEI_ei.svg
3 saved in  findEI_cdf.svg
```

```
1 saved in findEI_eq.svg
4 saved in findEI_v2.svg
```

which produces these plots:



In this example, the original expected inclination at paleolatitude of 42 (61°) is recovered within the 95% confidence bounds.

5.2.41 fisher.py

[Essentials Chapter 11] [fisher docs]

Draw a set of 10 directions from a Fisher distribution with a κ of 30 using **fisher.py**:

```
$ fisher.py -k 30 -n 10
233.7    81.4
357.0    76.4
272.5    62.8
137.0    70.0
83.7     71.2
...
```

You could plot the output with, e.g., eqarea.py.

Note that every instance of this program draws a different distribution, so yours will look different in detail.

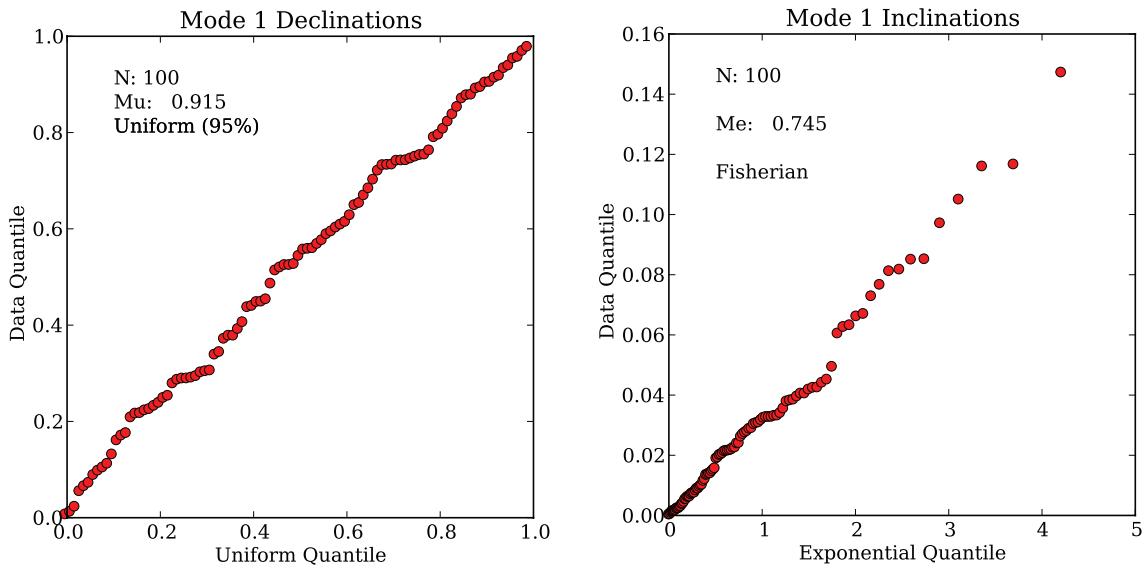
5.2.42 fishqq.py

[Essentials Chapter 11] [fishqq docs]

Test whether a set of 100 data points generated with fisher.py are in fact Fisher distributed by using a Quantile-Quantile plot:

```
$ fisher.py -k 30 -n 100 >fishqq_example.txt
$ fishqq.py -f fishqq_example.txt
```

produces these plots:



which support a Fisher distribution for these data.

5.2.43 fishrot.py

[Essentials Chapter 11] [fishrot docs]

Draw a set of 5 directions drawn from a Fisher distribution with a true mean declination of 33, a true mean inclination of 41, and a κ of 50:

```
$ fishrot.py -n 5 -D 33 -I 41 -k 50
 35.8   32.8
 36.2   30.2
 37.5   41.8
 28.6   23.9
 26.1   32.8
```

5.2.44 foldtest.py

[Essentials Chapter 12] [foldtest docs]

Use **foldtest.py** to perform the Tauxe and Watson (1994) foldtest on the data in *foldtest_example.dat*.

```
$ foldtest.py -f foldtest_example.dat
doing 1000 iterations...please be patient.....
0
```

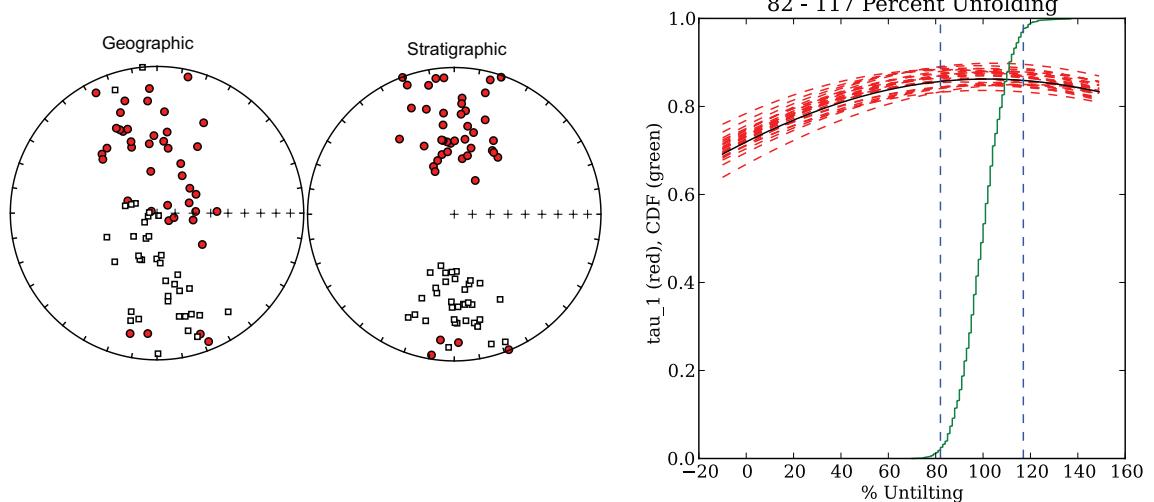
```

50
100
.
.
.

82 - 117 Percent Unfolding
range of all bootstrap samples: 70 - 137
S[a]ve all figures, <Return> to quit   a
3 saved in fold_ta.svg
2 saved in fold_st.svg
1 saved in fold_ge.svg

```

which gives the plots:



Apparently these directions were acquired prior to folding because the 95% confidence bounds on the degree of untilting required for maximizing concentration of the data (maximum in principle eigenvalue) τ_1 of orientation matrix (see the section on eigenvalues in the textbook) includes 100%.

5.2.45 foldtest_magic.py

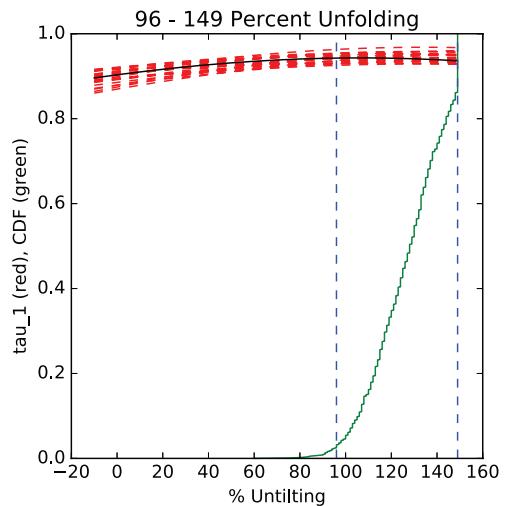
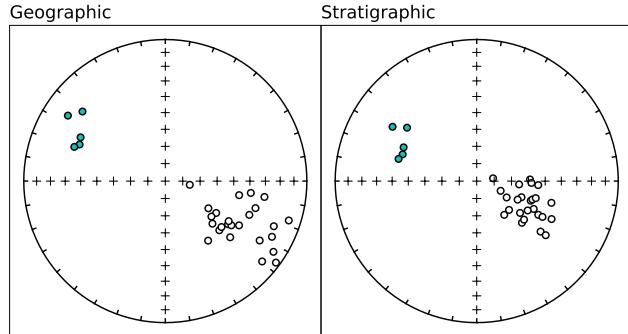
[Essentials Chapter 12] and [MagIC Database] [foldtest_magic docs]

This program performs the same test as foldtest.py. The only difference is that it reads MagIC formatted input files and allows the application of selection criteria as specified in the *pmag_criteria.txt* formatted file.

To begin, download the file from this references: Halls et al. (1974; doi: 10.1139/e74-113) at <https://earthref.org/MagIC/DOI/10.1139/e74-113> and unpack it with `download_magic.py`. Then run `foldtest_magic.py` for the fold test.

```
$ download_magic.py -f magic_contribution_11087.txt
$ foldtest_magic.py -f pmag_sites.txt -fsi er_sites.txt
doing 1000 iterations...please be patient.....
0
50
....
900
950
96 - 149 Percent Unfolding
S[a]ve all figures, <Return> to quit
a
3 saved in foldtest_ta.svg
2 saved in foldtest_st.svg
1 saved in foldtest_ge.svg
```

which gives the plots:



5.2.46 gaussian.py

[Essentials Chapter 11] [gaussian docs]

Use **gaussian.py** to generate a set of 100 normally distributed data points drawn from a population with a mean of 10.0 and standard deviation of 30. Save it to a file named **gauss.out**.

```
$ gaussian.py -s 3 -n 100 -m 10. -F gauss.out
```

You can check the sample mean and standard deviation with **stats.py** or make a histogram of the data with **histplot.py**

5.2.47 gobing.py

[Essentials Chapter 12] [gobing docs]

Use the dataset generated in the **eqarea_ell.py** example. Calculate Bingham parameters using **gobing.py** instead of within the plotting program:

```
$ gobing.py -f tk03.out
357.8    60.3     4.5   105.7    10.0     4.5    21.0   -27.6 20
```

which according to the help message from **gobing.py** is:

mean dec, mean inc, Eta, Deta, Ieta, Zeta, Zdec, Zinc, N

5.2.48 gofish.py

[Essentials Chapter 11] [gofish docs]

Draw a set of 10 directions drawn from a Fisher distribution with a true mean declination of 15, a true mean inclination of 41, and a κ of 50 and save it to a file, then use **gofish.py** to calculate the Fisher parameters:

```
$ fishrot.py -n 10 -D 15 -I 41 -k 50 >fishrot.out
$ gofish.py -f fishrot.out
10.8    39.6    10     9.8484    59.4     6.3    10.5
```

which according to the help message from **gofish.py -h** is: mean dec, mean inc, N, R, k, a95, csd. Your results will vary because every instance of **fishrot.py** draws a different sample from the Fisher distribution.

5.2.49 gokent.py

[Essentials Chapter 12] [gokent docs]

Draw a set of 20 data points from a TK03.GAD distribution predicted for a latitude of 42°N (see 14), without reversals. Calculate kent parameters using **gokent.py**

```
$ tk03.py -n 20 -lat 42 >tk03.out; gokent.py -f tk03.out
 359.2    55.0    9.3   147.7   30.8    7.8   246.8   14.9 20
```

which according to the help message from **gokent.py** is: mean dec, mean inc, Eta, Deta, Ieta, Zeta, Zdec, Zinc, N

5.2.50 goprinc.py

[Essentials Chapter 12] [goprinc docs]

Draw a set of 20 data points from a TK03.GAD distibution predicted for a latitude of 42°N (see 14), including reversals. Calculate the eigenparameters of the orientation matrix (the principal components) using **goprinc.py**

```
$ tk03.py -n 20 -lat 42 -rev >tk03.out; goprinc.py -f tk03.out
0.93863    11.0    58.6  0.04258   226.4    26.5  0.01879   128.3    15.6 20
```

which according to the help message from **goprinc.py** is: $\tau_1 V1_D, V1_I, \tau_2 V2_D V2_I \tau_3 V3_D V3_I, N$.

5.2.51 grab_magic_key.py

[MagIC Database] [grab_magic_key docs]

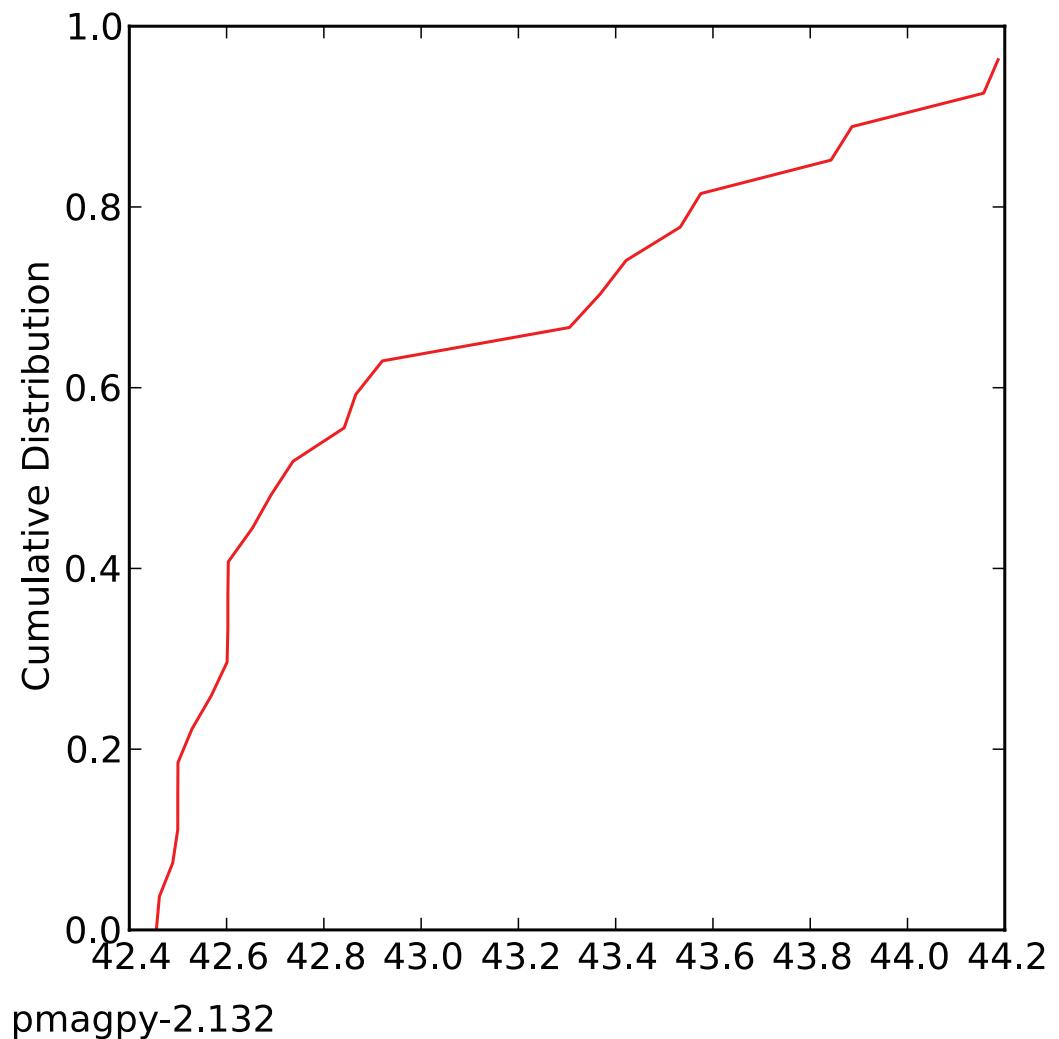
grab_magic_key.py is a utility that will print out any column (-key option) from any [MagIC Database] formatted file. For example, we could print out all the site latitudes from the *er_sites.txt* file down loaded in the download_magic.py example:

```
$ grab_magic_key.py -f er_sites.txt -key site_lat
42.60264
42.60264
42.60352
42.60104
...
```

You could save the data in a file with the output redirect function (>) and plot them with, say *plot_cdf.py*.

```
$ grab_magic_key.py -f er_sites.txt -key site_lat > lats
$ plot_cdf.py -f lats
```

which produces the fascinating (NOT!) plot:



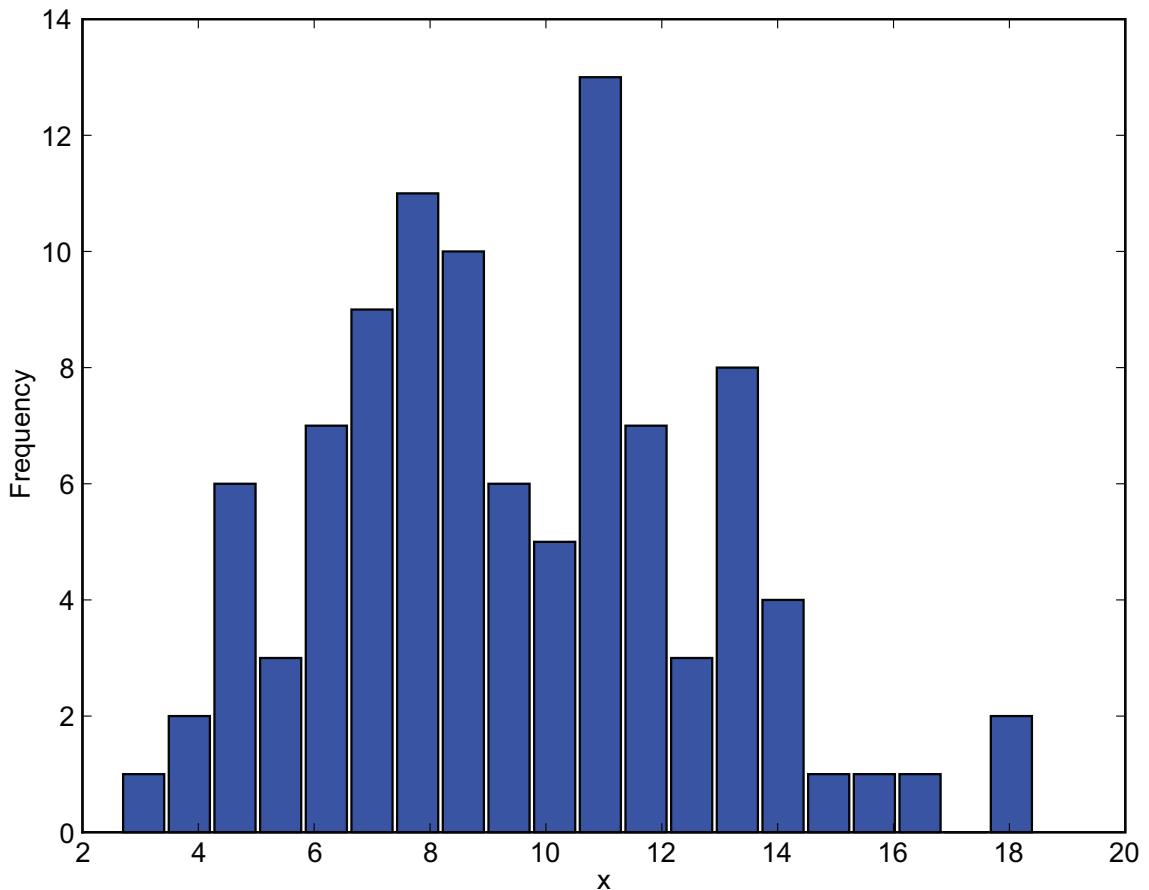
5.2.52 histplot.py

[histplot docs]

Make a histogram of the data generated with the **gaussian.py** program.

```
$ histplot.py -f gauss.out
```

which makes a plot similar to:



5.2.53 hysteresis_magic.py

[Essentials Chapters 5], [Essentials Chapter 7], [Essentials Appendix C.1] & [MagIC Database] [hysteresis_magic docs]

Plot the data in *hysteresis_magic_example.txt*, (from Ben-Yosef et al., 2008) which were imported into MagIC using AGM_magic.py. Use the program **hysteresis_magic.py** to plot the data.

```
$ hysteresis_magic.py -f hysteresis_magic_example.dat

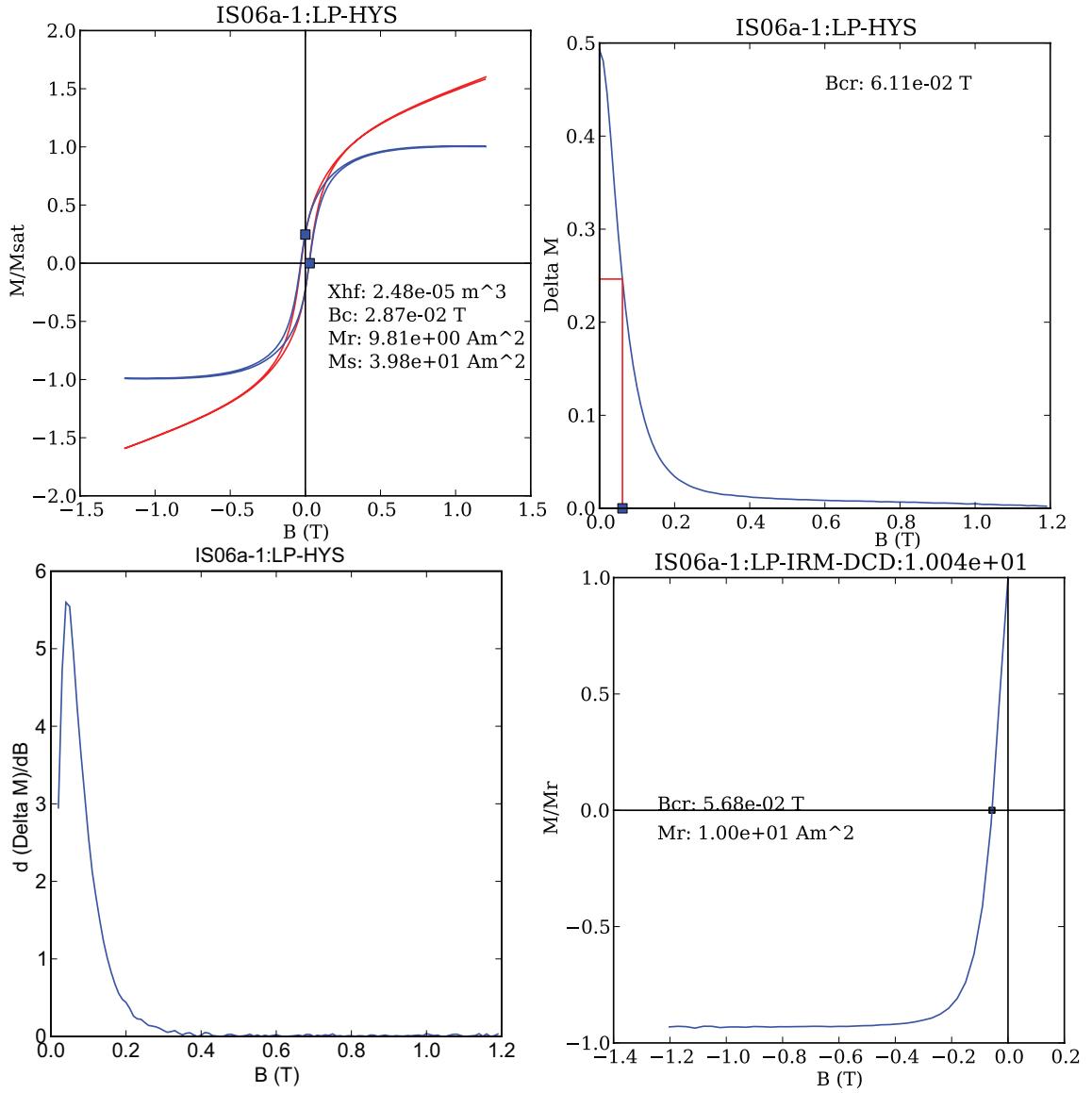
IS06a-1 1 out of  8
S[a]ve plots, [s]pecimen name, [q]uit, <return> to continue
a
1 saved in _IS06a-1_hyst.svg
```

```

3 saved in _IS06a-1_DdeltaM.svg
2 saved in _IS06a-1_deltaM.svg
5 saved in _IS06a-1_irm.svg

```

which makes the plots:



5.2.54 igrf.py

[Essentials Chapter 2][Essentials Chapter 2] [igrf docs]

Use the program **igrf.py** to estimate the field on June 1, 1995 in Amsterdam, The Netherlands (52.5° N, 5° E).

```
$ igrf.py -i
Decimal year: <cntrl-D to quit> 1995.5
Elevation in km [0]
Latitude (positive north) 52.5
Longitude (positive east) 5
    357.9    67.4    48534

Decimal year: <cntrl-D to quit> ^D
Good-bye
```

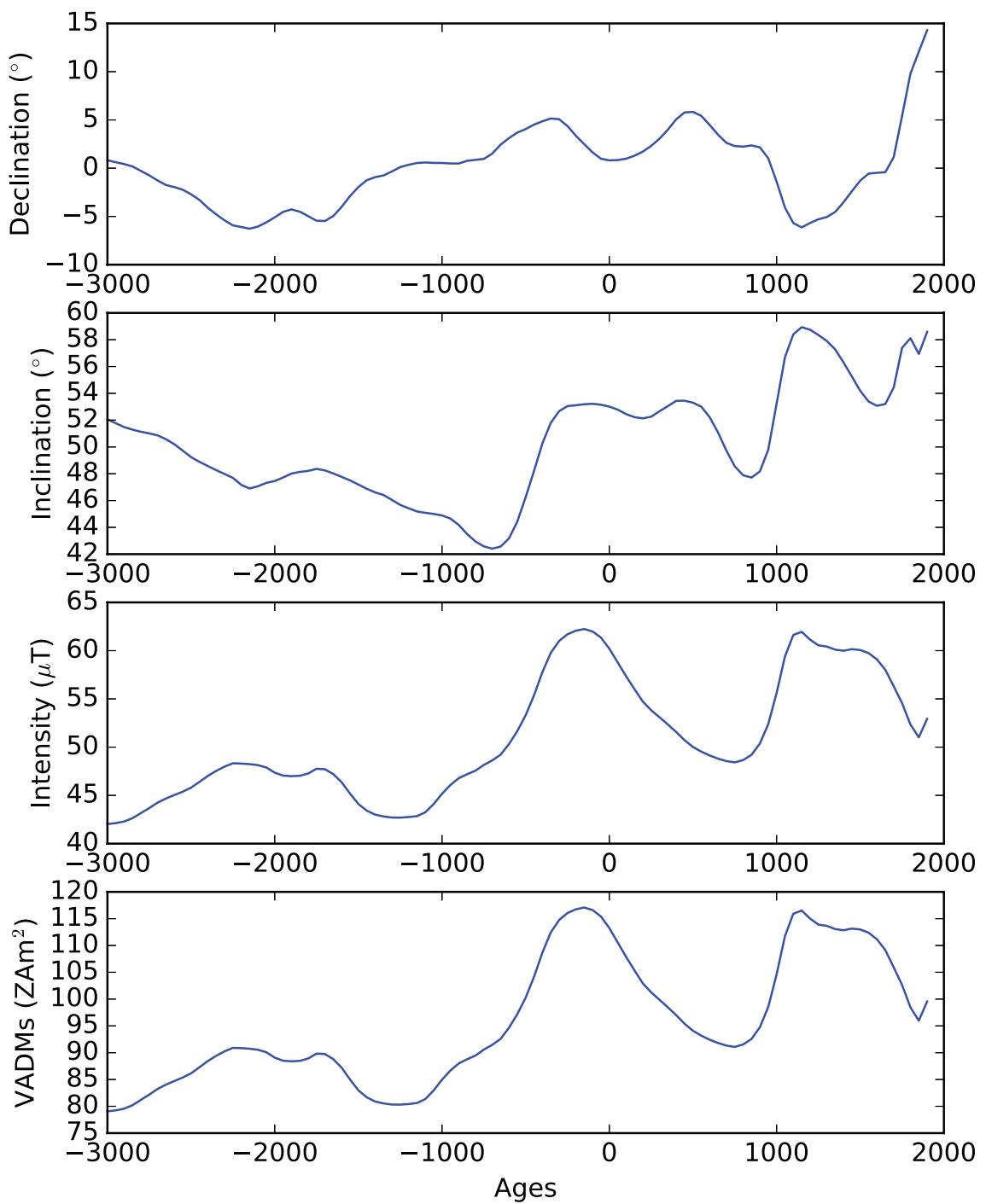
Now read from the file *igrf_example.dat* which requests field information for near San Diego for the past 3000 years. The program will evaluate the field vector for that location for dates from 1900 to the present using the IGRF/DGRF coefficients in the IGRF-11 model available from: <http://www.ngdc.noaa.gov/IAGA/vmod/igrf.html>. For the period from 1000 BCE to 1800, the program uses the CALS3k.4b of Korte and Constable (2011) available at: <http://earthref.org/ERDA/1142/>. Prior to that and back to 8000 BCE, the program uses the coefficients of Korte et al., 2011 for the CALS10k.1b, available at: <http://earthref.org/ERDA/1403/>

```
$ igrf.py -f igrf_example.dat -F igrf.out
```

You can also make a plot of secular variation of field elements by specifying the age range and location on the command line. Try this for the location of San Diego for the age range: -3000 1925 in increments of 50 years:

```
$ igrf.py -ages -3000 1950 50 -loc 33 -117 -mod pfm9k -plt
S[a]ve to save figure, <Return> to quit
```

and get this plot:



5.2.55 install_etopo.py

Some mapping utilities use the Etopo package for topography and these data sets do not come standard with the Python installation. To install these properly, simply type:

```
$ install_etopo.py
```

5.2.56 incfish.py

[Essentials Chapter 11] [incfish docs]

Use the program **incfish.py** to calculate average inclination for inclination only data simulated by fishrot.py for an average inclination of 60°. If you save the declination, inclination pairs, you can compare the **incfish.py** answer with the Fisher mean. The datafile *incfish_example_di.dat* has the declination, inclination pairs and *incfish_example_inc.dat* has just the inclinations.

```
$ fishrot.py -I 60 -k 10 > incfish_example_di.dat
$ awk '{print $2}' incfish_example_di.dat > incfish_example_inc.dat
$ incfish.py -f incfish_example_inc.dat
    57.1    61.0   100    92.9    13.9     1.0
$ gofish.py -f incfish_example_di.dat
    1.8    62.9   100   91.2727   11.3     4.4    24.0
```

The output for **incfish.py** is: [gaussian] mean inc, Fisher inc, N , R , k , α_{95} . You can see that the **incfish.py** result is much closer to the Fisherian result than the gaussian mean is.

5.2.57 irmaq_magic.py

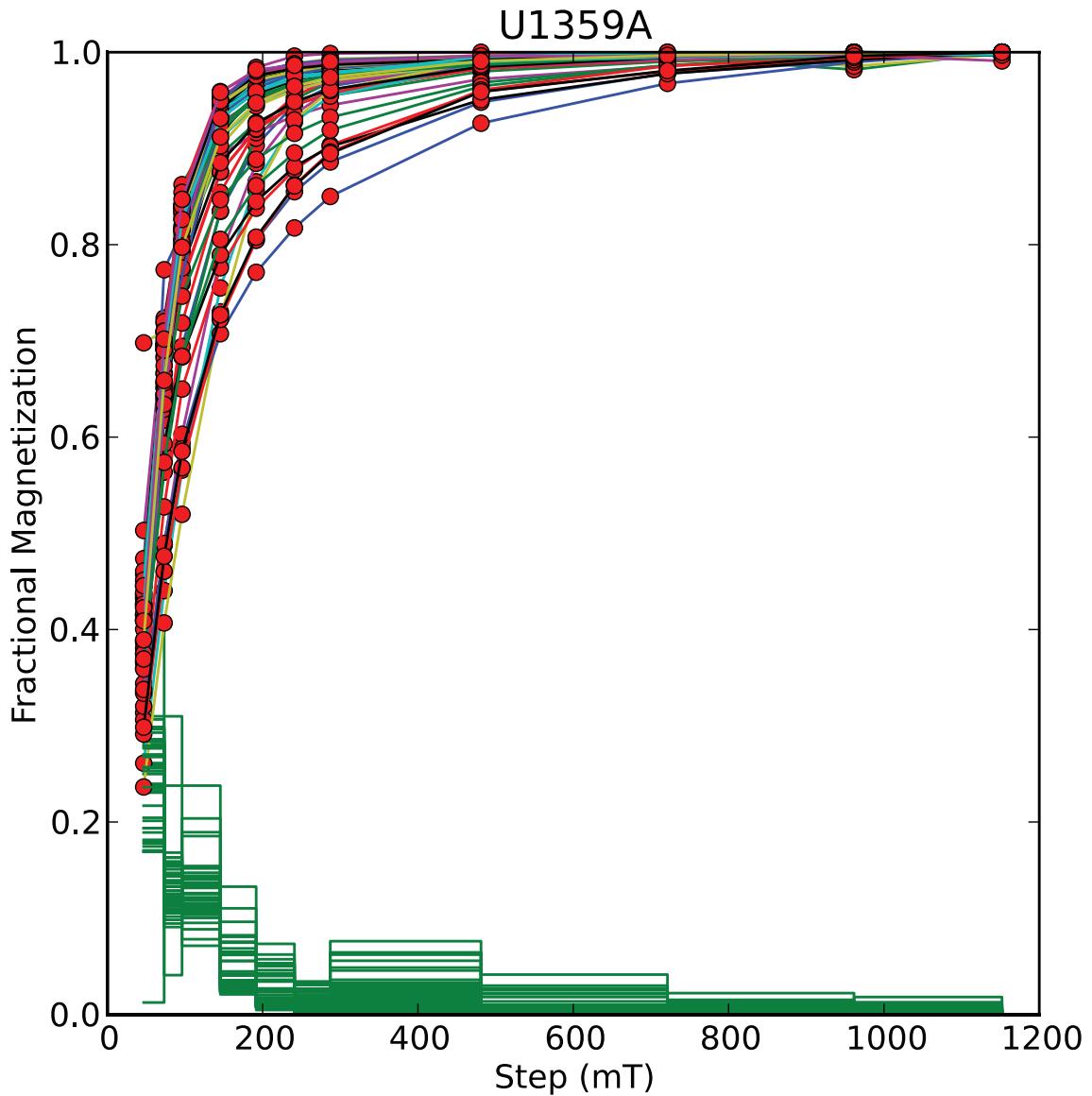
MagIC [irmaq_magic docs]

Someone (Saiko Sugisaki) measured a number of samples from IODP Expedition 318 Hole U1359A for IRM acquisition curves. She used the ASC impulse magnetizer's coils # 2 and 3 and saved the data in the SIO format. Convert these to the MagIC measurements format, combine them in a single *magic_measurements.txt* file with *combine_magic.py* and plot the data with **irmaq_magic.py**.

```
$ sio_magic.py -f U1359A_IRM_coil2.txt -LP I -V 2 -F U1359A_IRM_coil2.magic \
    -loc U1359A -spc 0 -ncn 5
$ sio_magic.py -f U1359A_IRM_coil3.txt -LP I -V 3 -F U1359A_IRM_coil3.magic \
```

```
-loc U1359A -spc 0 -ncn 5
$ combine_magic.py -F magic_measurements.txt -f U1359A_IRM_coil2.magic \
U1359A_IRM_coil3.magic
$ irmaq_magic.py
559 records read from magic_measurements.txt
U1359A
S[a]ve to save plot, [q]uit, Return to continue: a
1 saved in U1359A_LP-IRM.svg
```

which produces the plot:



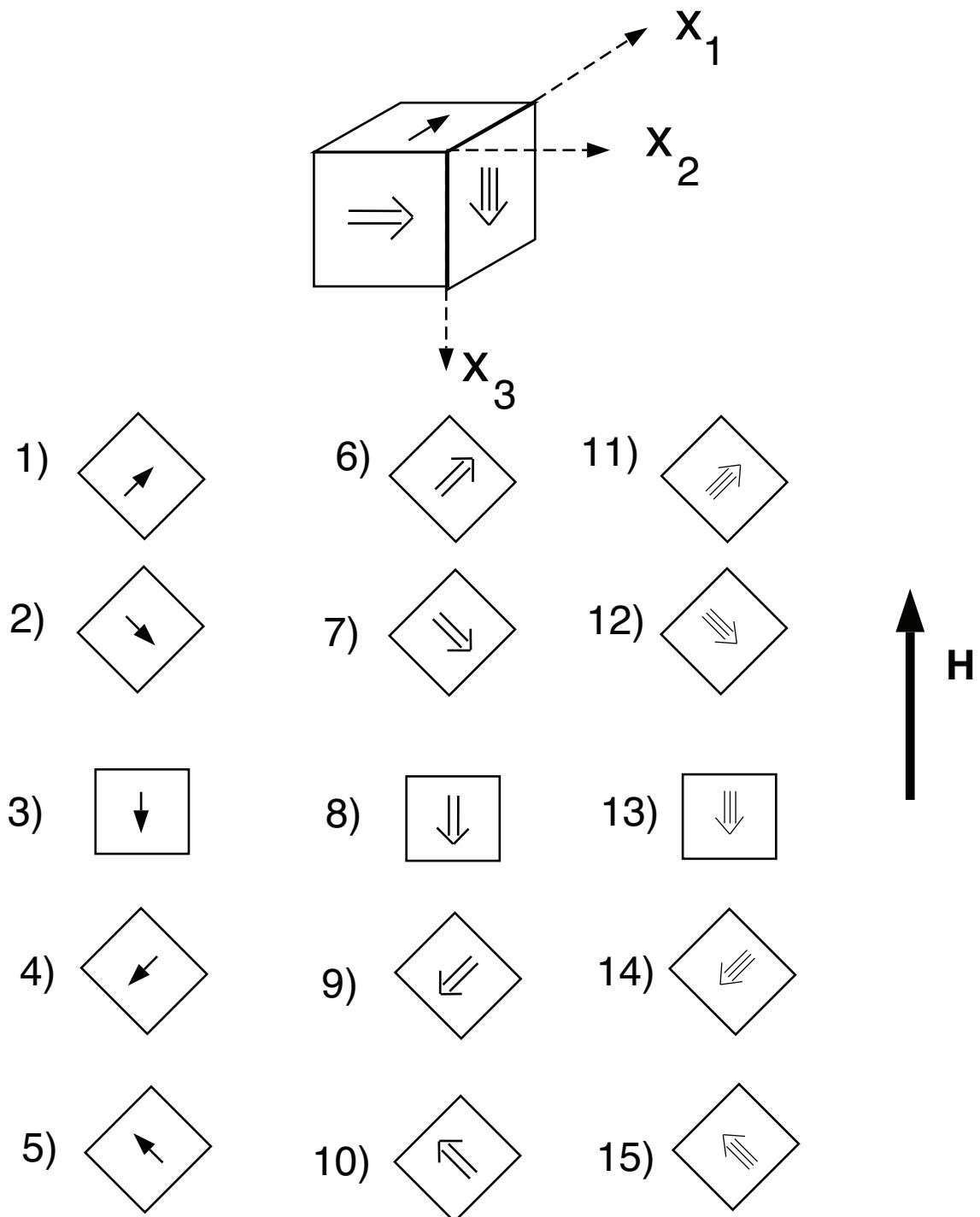
5.2.58 k15_magic.py

[Essentials Chapter 13]; [MagIC Database] [k15_magic docs]

Someone took a set of samples from a dike margin in the Troodos Ophiolite and measured their anisotropy of magnetic susceptibility on a Kappabridge KLY 2.0 instrument in the SIO laboratory:

tr245f	80.00	-46.0	204	25
995.	999.	993.	995.	1000.
1004.	999.	1001.	1004.	999.
998.	997.	1002.	998.	997.
tr245g	52.00	-23.0	204	25
1076.	1066.	1072.	1077.	1067.
1076.	1068.	1072.	1076.	1067.
1068.	1075.	1071.	1068.	1076.
tr245h	123.00	-29.0	204	25
1219.	1231.	1218.	1220.	1232.
1230.	1231.	1234.	1230.	1231.
1221.	1221.	1225.	1221.	1221.
tr245i1	68.00	-26.0	204	25
1031.	1027.	1025.	1032.	1028.
1035.	1031.	1035.	1035.	1032.
1030.	1027.	1032.	1030.	1027.

The first line of each set of four has the specimen name, azimuth, plunge, and bedding strike and dip the next three lines are sets of five measurements in the 15 positions recommended by Jelinek (1977):



The 15 measurements for each specimen, along with orientation information and the specimen name were saved in the file *k15_example.dat*. Convert these to the MagIC format using the program **k15_magic.py**:

```
$ k15_magic.py -spc 0 -f k15_example.dat -loc "Troodos Ophiolite"
Data saved to: ./er_samples.txt ./rmag_anisotropy.txt ./rmag_results.txt ./k15_r...
```

You can plot the output of this example (default file *rmag_anisotropy.txt*) using the program **aniso_magic.py**.

5.2.59 k15_s.py

[Essentials Chapter 13]; [MagIC Database] [[k15_s docs](#)]

Use **k15_s.py** to calculate the best-fit tensor elements and residual error for the data in the file *k15_example.dat* (same file as for *k15_magic.py*). These are: the specimen name, azimuth and plunge and the strike and dip, followed by the 15 measurements made using the Jelinek 1977 scheme shown in the *k15_magic.py* example. Calculate the .s data in specimen, geographic and tilt adjusted coordinates:

```
$ k15_s.py -f k15_example.dat
0.33146986 0.33413991 0.33439023 0.00075095 -0.00083439 -0.00016688 0.00008618
0.33335925 0.33335925 0.33328149 -0.00155521 -0.00132193 0.00116641 0.00017193
0.33097634 0.33573565 0.33328801 0.00163177 0.00013598 0.00000000 0.00018131
...
$ k15_s.py -f k15_example.dat -crd g
0.33412680 0.33282733 0.33304587 -0.00015289 0.00124840 0.00135721 0.00008618
0.33556300 0.33198264 0.33245432 0.00087259 0.00024141 0.00096166 0.00017193
0.33584908 0.33140627 0.33274469 0.00131844 0.00118816 0.00002987 0.00018131
...
$ k15_s.py -f k15_example.dat -crd t
0.33455712 0.33192658 0.33351630 -0.00043563 0.00092770 0.00105006 0.00008618
0.33585501 0.33191562 0.33222935 0.00055960 -0.00005314 0.00064730 0.00017193
0.33586666 0.33084926 0.33328408 0.00142269 0.00013235 0.00009201 0.00018131
...
```

5.2.60 KLY4S_magic.py

[Essentials Chapter 13]; [MagIC Database] [[KLY4S_magic docs](#)]

The program **AMSSpin** available for downloading from <http://earthref.org/ERDA/940/> generates data for the Kappabridge KLY4S spinning magnetic susceptibility instrument as described by Gee et al. (2008).

The files have the format:

```
318-U1359B-011H-1-W-75 0.3415264 0.3403534 0.3181202 -0.0006608 0.0000948 0.0023186 2.2
318-U1359B-011H-2-W-76 0.3369955 0.3361130 0.3268916 0.0000845 -0.0005236 0.0003290 3.5
318-U1359B-011H-3-W-78 0.3373485 0.3364144 0.3262371 -0.0002281 0.0005881 -0.0011413 3.5
318-U1359B-011H-4-W-96 0.3343428 0.3323376 0.3333195 0.0007210 -0.0005503 0.0011256
```

where the columns are:

Specimen S_1 S_2 S_3 S_4 S_5 S_6 χ_b (μ SI) date time user

Output files are in the format of the file *KLY4S_magic_example.dat* (found in the Measurement_Import/KLY4S_magic folder). One option is for orientation information to be output as an *azdip* formatted file (see *azdip_magic.py*). Try it out on some data from IODP Expedition 318 (Hole U1359B) published by Tauxe et al., (2012). Note that the sample naming convention is # 5 (-ncn 5) and the sample name is the same as the site (-spc 0) using **KLY4S_magic.py** as follows:

```
%KLY4S_magic.py -f KLY4S_magic_example.dat -spc 0 -ncn 5
```

This command will create the files needed by the MagIC database and the data can be plotted using **aniso_magic.py**. If you were to import the sample files from the LIMS data base for these samples, you could plot them versus depth, or as equal area projections using **ANI_depthplot.py** and **aniso_magic.py** respectively.

5.2.61 lnp_magic.py

[Essentials Chapter 11], [Essentials Appendix C2.2] & [MagIC Database] [*lnp_magic* docs]

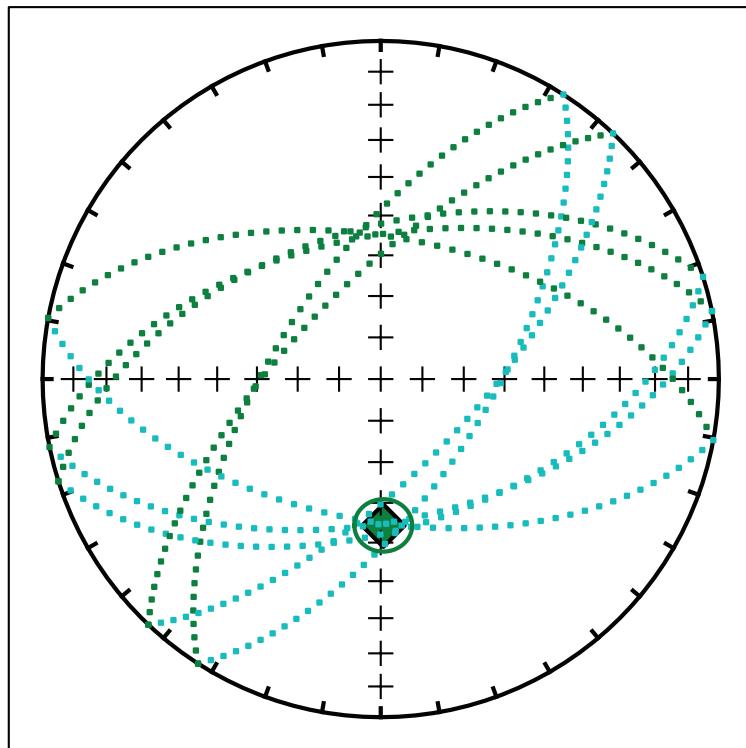
This program will take *pmag-specimen* formatted MagIC files (for example, generated by *zeq_magic.py*) and plot data by site, combining best-fit lines and best-fit planes using the method described in Essentials Appendix C2.2. Try this out on the data from the San Francisco Volcanics, notorious for lightning strikes, published by Tauxe et al., 2003. These can be downloaded from the MagIC database from <http://earthref.org/MAGIC/m000629dt20061213090720/> and unpacked with *download_magic.py*.

```
$ download_magic.py -f zmab0001193tmp02.txt
```

```
working on: 'er_locations'
er_locations data put in ./er_locations.txt
working on: 'er_sites'
er_sites data put in ./er_sites.txt
working on: 'er_samples'
er_samples data put in ./er_samples.txt
...
$ lnp_magic.py -f pmag_specimens.txt -crd g
sv01
Site lines planes kappa a95 dec inc
sv01 0 5 286 6.6 179.0 -54.3 4.9948
$ tilt correction: 0
s[al]ve plot, [q]uit, <return> to continue:
a
1 saved in sv01_g_eqarea.svg
```

which generated this figure:

sv01: geographic coordinates



5.2.62 lowrie.py

[Essentials Chapter 8] [lowrie docs]

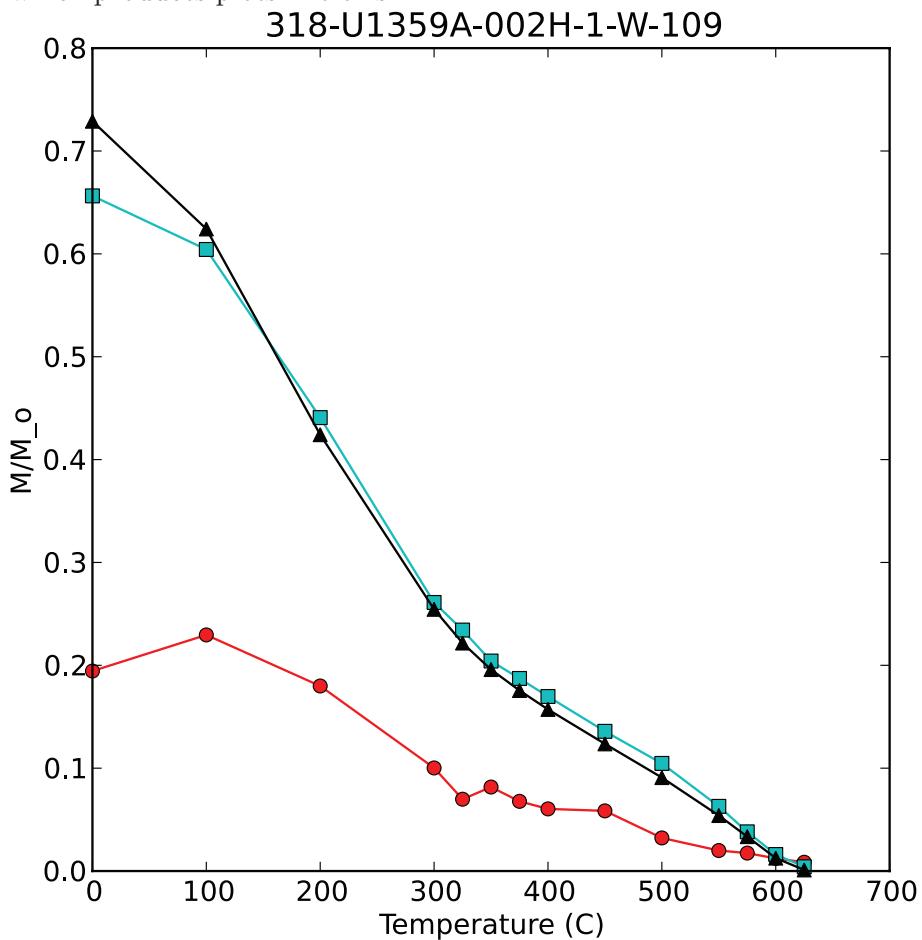
Someone (Saiko Sugisaki) subjected a number of specimens from IODP Expedition 318 Hole U1359A specimens to a 3-D IRM experiment and saved the data in the SIO format. Use **lowrie.py** to make plots of blocking temperature for the three coercivity fractions.

```
$ lowrie.py -f lowrie_example.dat
318-U1359A-002H-1-W-109
S[ave figure? [q]uit, <return> to continue  a
1  saved in  lowrie:_318-U1359A-002H-1-W-109_.svg
```

318-U1359A-002H-4-W-65

S[a]ve figure? [q]uit, <return> to continue q

which produces plots like this:



5.2.63 lowrie_magic.py

[Essentials Chapter 8] and [MagIC Database] [lowrie_magic docs]

This program works exactly like lowrie.py, but works on *magic_measurements.txt* formatted files. Use sio_magic.py to import the *lowrie_example.dat* data file into the MagIC format. Then use **lowrie_magic.py** to plot the data:

```
$ sio_magic.py -f lowrie_example.dat -LP I3d -loc U1359A -F lowrie_magic_example
averaging: records 11 12
```

```
318-U1359A-004H-2-W-18 started with 15 ending with 14
Averaged replicate measurements
averaging: records 13 14
318-U1359A-004H-2-W-44 started with 15 ending with 14
Averaged replicate measurements
averaging: records 14 16
318-U1359A-012H-5-W-70 started with 16 ending with 14
Averaged replicate measurements
averaging: records 14 15
$ lowrie_magic.py -f lowrie_magic_example.dat
318-U1359A-002H-1-W-109
S[a]ve figure? [q]uit, <return> to continue
```

5.2.64 magic_select.py

[MagIC Database] [magic_select docs]

This program takes any MagIC formatted file and selects lines that match the search criteria and saves the output as a new MagIC formatted file of the same type. Selection criteria match whole or partial strings, avoid whole or partial strings or evaluate minimum or maximum values. The syntax is to specify the input file with the -f option, the key you wish to search on with -key, followed by the string you wish to use as a criterion, followed with a 'T' for match exactly, 'F' avoid entirely, 'has' for matching partially and 'not' for avoiding any partial match, and min, max and eval for evaluating the numerical value. The -F option sets the output file.

For example, you could pick out all the records that match a certain site name string. You could select out records with specified method codes. You could get all records with inclinations that are positive.

Use **magic_select.py** to pick out all the best-fit lines based on AF demagnetization data from the *pmag-specimens.txt* file unpacked from the MagIC database in the download_magic.py example.

```
$ magic_select.py -f pmag_specimens.txt -key magic_method_codes LP-DIR-AF has -F AF_specimens.txt
76 records written to ./AF_specimens.txt
$ magic_select.py -f AF_specimens.txt -key magic_method_codes DE-BFL has -F AF_BFL_specimens.txt
69 records written to ./AF_BFL_specimens.txt
```

5.2.65 make_magic_plots.py

[MagIC Database] [make_magic_plots docs]

This program will inspect the files in the current directory and autogenerate some standard plots.

5.2.66 Measurement Import Scripts

2G_bin_magic.py

[2G_bin_magic.py docs]

This program imports the binary format generated by the 2G proprietary software. It will place the orientation information in the er_samples.txt file and er_sites.txt file by default. Naming and orientation conventions can be specified as in the sections on Naming conventions and Orientation conventions. You can also specify sampling method codes that pertain to ALL samples (see section on field information.)

AGM_magic.py

[Essentials Chapter 5] & [MagIC Database] [AGM_magic docs]

This program imports Micromag hysteresis files into magic_measurements formatted files. Because this program imports data into the MagIC database, specimens need also to have sample/site/location information which can be provided on the command line. If this information is not available, for example if this is a synthetic specimen, specify -syn SYN_NAME for synthetic on the command line instead of the -spn SPEC_NAME switch.

Someone named Lima Tango has measured a synthetic specimen named *myspec* for hysteresis and saved the data in a file named *agm_magic_example.agm*. The backfield IRM curve for the same specimen was saved in *agm_magic_example.irm*. Use the program **AGM_magic.py** to import the data into a magic_measurements formatted output file. These were measured using cgs units, so be sure to set the units switch properly. Combine the two output files together using *combine_magic.py*. [This can be plotted using **hysteresis_magic.py** or **quick_hyst.py**.] **hysteresis_magic.py** will calculate various hysteresis parameters and put them in the relevant magic tables for you.] s

```
$ AGM_magic.py -spn myspec --usr "Lima Tango" -f agm_magic_example.agm -u cgs
results put in ./agm_measurements.txt
$ AGM_magic.py -spn myspec --usr "Lima Tango" -f agm_magic_example.irm -u cgs
```

```
results put in ./irm_measurements.txt
$ combine_magic.py -F magic_measurements.txt -f agm_measurements.txt irm_measurements.txt
```

CIT_magic.py

[CIT_magic.py docs]

Craig Jones' **PaleoMag** software package (<http://cires.colorado.edu/people/jones.craig/PMag3.html>) imports various file formats, including the so-called 'CIT' format developed for the Cal Tech lab. The documentation for the CIT sample format is here: http://cires.colorado.edu/people/jones.craig/PMag_Formats.html#SAM_format. Demagnetization data for each specimen is in its own file in a directory with all the data for a study. These files are rather strictly formatted with fields determined by the character number in the line. A typical datafile (hat tip Swanson-Hysell et al. (2009)) has this format:

```
MP 18-1
-----169.0 47.0 170.0 42.0 1.0
NRM 256.8 -60.3 63.7 -77.5 4.36E-03 001.8 351.8 -72.5 3.244495 13.18438 0.620611 lower
TT 254.0 -60.5 70.1 -77.5 4.28E-03 002.3 356.4 -72.5 4.752208 16.68586 1.969320 shoe
AF 260.3 -60.5 56.5 -76.8 4.32E-03 000.6 346.6 -71.8 3.370241 2.506036 0.391227 lower
AF 20 256.4 -61.0 65.2 -76.8 4.33E-03 000.5 352.9 -71.8 3.260177 2.374987 0.277467 lower
AF 40 254.1 -61.3 70.0 -76.7 4.34E-03 000.8 356.4 -71.7 3.283688 5.443790 0.216938 lower
TT 100 254.6 -61.6 69.1 -76.4 4.36E-03 002.6 355.8 -71.3 1.512697 20.08180 0.568813 shoe
TT 150 259.5 -61.8 59.9 -75.7 4.49E-03 000.6 349.0 -70.6 2.292811 4.155307 0.582492 shoe
TT 200 254.2 -62.5 70.2 -75.4 4.57E-03 000.7 356.7 -70.4 3.548058 4.420838 1.117214 shoe
TT 250 255.4 -62.5 68.0 -75.4 4.59E-03 000.9 355.1 -70.4 5.709379 4.016543 2.128517 shoe
TT 300 254.3 -63.7 70.4 -74.3 4.55E-03 001.3 356.9 -69.2 4.430973 9.541593 1.820396 shoe
TT 350 254.9 -64.5 69.6 -73.5 4.49E-03 000.8 356.3 -68.4 2.008315 6.203830 0.690625 shoe
TT 400 252.8 -64.2 72.8 -73.8 4.48E-03 001.6 358.8 -68.8 2.923507 12.20715 1.171037 shoe
```

There is an optional first line with 'CIT' on it (not shown here).

There must be a file with the suffix '.sam' in the same directory which gives details about the samples and a list of the data files in the directory. The .sam file has the form:

```
Mamainse Point
47.1 275.3 -7.2
MP18-1
MP18-2
MP18-3
```

MP18-4
 MP18-5
 MP18-6

The first line is a comment, the second is the latitude and longitude followed by a declination correction.

For detailed description of the file format, check the PaleoMag home page.

Use the program **CIT_magic.py** to import the data files from the example data files in the *CIT_magic* directory of the *Measurement_Import* directory of the *data_files* directory. The location name was “Mamainse Point”, the naming convention was #2 and they were collected by drilling and with a magnetic compass.

```
CIT_magic.py -f bMP.sam -loc "Mamainse Point" -spc 0 -ncn 2 -mcd 'FS-FD:SO-M'
Mamainse Point first run (samples collected 10/05, samples run 04/06)

specimens stored in ./er_specimens.txt
samples stored in ./er_samples.txt
averaging: records 1 3
MP18-1 started with 23 ending with 21
Averaged replicate measurements
averaging: records 1 2
MP18-2 started with 25 ending with 24
Averaged replicate measurements
averaging: records 1 3
MP18-3 started with 26 ending with 24
Averaged replicate measurements
averaging: records 1 2
MP18-4 started with 25 ending with 24
Averaged replicate measurements
averaging: records 1 3
MP18-5 started with 26 ending with 24
Averaged replicate measurements
averaging: records 1 2
MP18-6 started with 25 ending with 24
Averaged replicate measurements
data stored in ./magic_measurements.txt
```

These data can now be viewed and interpreted using, for example *zeq_magic.py*.

generic_magic.py

[generic_magic.py docs]

If you have a data file format that is not supported, you can relabel column headers to fit the generic format in *generic_magic.py*:

specimen	treatment	treatment-type	moment	dec_s	inc_s
sr01e2	0	A	2.93E-02	200.6	27.9
sr01e2	10	A	2.83E-02	201	27.7
sr01e2	20	A	2.61E-02	200.5	27.4
sr01e2	30	A	2.37E-02	199.9	27.7
sr01e2	60	A	1.85E-02	202.5	27.9

For more options, here is the help message for **generic_magic.py** :

A generic file is a tab-delimited file. Each columns should have a header.
The file must include the follwing headers (the order of the columns is not impor-

```

specimen
    string specifying specimen name

treatment:
    a number with one or two decimal point (X.Y)
    coding for thermal demagnetization:
        0.0 or 0 is NRM.
        X is temperature in celcsius
        Y is always 0
    coding for AF demagnetization:
        0.0 or 0 is NRM.
        X is AF peak field in mT
        Y is always 0
    coding for Thellier-type experiment:
        0.0 or 0 is NRM
        X is temperature in celcsius
        Y=0: zerofield
        Y=1: infiel
        Y=2: pTRM check
        Y=3: pTRM tail check
        Y=4: Additivity check
        # Ron, Add also 5 for Thellier protocol

```

```

treatment_type:
    N: NRM
    A: AF
    T: Thermal

moment:
    magnetic moment in emu !!

```

In addition, at least one of the following headers are required:

```

dec_s:
    declination in specimen coordinate system (0 to 360)
inc_s:
    inclination in specimen coordinate system (-90 to 90)

dec_g:
    declination in geographic coordinate system (0 to 360)
inc_g:
    inclination in geographic coordinate system (-90 to 90)

dec_t:
    declination in tilt-corrected coordinate system (0 to 360)
inc_t:
    inclination in tilt-corrected coordinate system (-90 to 90)

```

This program is called within Pmag GUI but could be used as a stand alone program if you wish.

HUJI_magic.py

[HUJI_magic.py docs]

This program was developed for the late Prof. Hagai Ron at the Hebrew Universisty, Jerusalem for files with formats like this:

```

mk118 07R-08329 5/10/2007 7:35 N 0 10.4 73.9 10.4 73.9 2.23E-03
mk118 07R-08330 5/10/2007 7:37 A 5 359.2 60 359.2 60 2.19E-03
mk118 07R-08331 5/10/2007 7:38 A 10 358.4 48 358.4 48 1.50E-03
mk118 07R-08332 5/10/2007 7:40 A 15 357.7 43.5 357.7 43.5 8.34E-04
mk118 07R-08333 5/10/2007 7:42 A 20 358.4 42.5 358.4 42.5 4.89E-04
mk118 07R-08334 5/10/2007 7:44 A 25 358.8 40.6 358.8 40.6 3.06E-04

```

```

mk118 07R-08335 5/10/2007 7:46 A 30 356.6 41.1 356.6 41.1 2.16E-04
mk118 07R-08336 5/10/2007 7:48 A 40 357 39.3 357 39.3 1.39E-04
mk118 07R-08337 5/10/2007 7:50 A 50 357 40 357 40 1.03E-04
mk118 07R-08338 5/10/2007 7:53 A 60 351.7 46.9 351.7 46.9 9.64E-05
mk118 07R-08339 5/10/2007 7:55 A 70 350.7 48.7 350.7 48.7 8.89E-05
mk118 07R-08340 5/10/2007 7:58 A 80 353.8 38.8 353.8 38.8 6.77E-05

```

HUJI_magic.py works in a similar fashion to **sio_magic.py**.

LDEO_magic.py

[MagIC Database] [LDEO_magic docs]

This program works in much the same fashion as **sio_magic.py** but the file formats are different. Here is a typical example:

```

isaf2.fix
LAT:   .00  LON:   .00
      ID    TREAT   I   CD     J    CDECL CINCL  GDECL GINCL  BDECL BINCL  SUSC  M/V
-----
is031c2       .0  SD  0 461.600 163.9  17.5  337.1  74.5  319.1  74.4   .0   .0

```

The first line is the file name and the second has the latitude and longitude information. The columns are:

```

ID: specimen name
TREAT: treatment step
I: Instrument
CD: Circular standard deviation
J: intensity. assumed to be total moment in 10^-4 (emu)
CDECL: Declination in specimen coordinate system
CINCL: Declination in specimen coordinate system
GDECL: Declination in geographic coordinate system
GINCL: Declination in geographic coordinate system
BDECL: Declination in bedding adjusted coordinate system
BINCL: Declination in bedding adjusted coordinate system
SUSC: magnetic susceptibility (in micro SI)a
M/V: mass or volume for nomalizing (0 won't normalize)

```

Use the program to import the file *ldeo_magic_example.dat* into the MagIC format. It was an AF demagnetization experiment.

```
$ LDEO_magic.py -f ldeo_magic_example.dat -LP AF
results put in magic_measurements.txt
```

IODP_csv_magic.py

Just for fun, download the whole core data from IODP expedition 318, Site U1359, Hole A. (Section Half set to 'A') from the IODP LIMS database using WebTabular. These data were used in Tauxe et al. (2012) after some editing (removal core ends and disturbed intervals). Convert them into the MagIC format using **ODP_csv_magic.py**:

```
$ IODP_csv_magic.py -f SRM_318_U1359_A_A.csv
processing:  SRM_318_U1359_A_A.csv
specimens stored in ./er_specimens.txt
samples stored in ./er_samples.txt
.....
Averaged replicate measurements
data stored in ./magic_measurements.txt
```

This takes a while so be patient....

You can also downloaded the core summary data from the LIMS database and convert it to the MagIC format using Pmag GUI. Now you can plot the data and the core tops using core_depthplot.py

PMD_magic.py

[PMD_magic.py docs]

This format is the one used to import .PMD formatted magnetometer files (used for example in the PaleoMac software of Cogné, 2003) into the MagIC format. (See <http://www.ipgp.fr/~cogne/pub/paleomac/PMhome.html> for the PaleoMac home page. The version of these files that **PMD_magic.py** expects (UCSC version) contains demagnetization data for a single specimen and have a format like this:

```
Strat post corrected - Summit Springs, -
ss0101a  a= 93.9  b= 61.0  s= 0.0  d= 0.0  v=11.0E-6m3  06/17/2003 12:00
STEP  Xc [Am2]  Yc [Am2]  Zc [Am2]  MAG[A/m]  Dg  Ig  Ds  Is  a95
H000 -7.46E-06 -1.61E-05 +5.31E-05 +5.09E+00  73.3  35.2  73.3  35.2  0.5  cryoS
H002 -7.57E-06 -1.53E-05 +5.03E-05 +4.83E+00  73.2  35.7  73.2  35.7  0.7  cryoS
H005 -7.35E-06 -1.16E-05 +3.62E-05 +3.52E+00  71.5  38.3  71.5  38.3  0.7  cryoS
H008 -7.35E-06 -6.27E-06 +1.92E-05 +1.95E+00  68.5  47.1  68.5  47.1  0.7  cryoS
H012 -6.84E-06 -3.32E-06 +1.20E-05 +1.29E+00  69.1  56.1  69.1  56.1  0.6  cryoS
H018 -6.00E-06 -2.26E-06 +8.96E-06 +1.00E+00  69.3  60.5  69.3  60.5  0.6  cryoS
H025 -5.16E-06 -1.74E-06 +7.18E-06 +8.19E-01  69.2  62.5  69.2  62.5  0.5  cryoS
```

```
H050 -3.12E-06 -9.23E-07 +4.03E-06 +4.71E-01 69.3 64.6 69.3 64.6 0.5 cryoSlug
H090 -1.80E-06 -5.32E-07 +2.23E-06 +2.65E-01 67.6 65.6 67.6 65.6 0.5 cryoSlug
H180 -9.49E-07 -2.94E-07 +1.21E-06 +1.42E-01 67.7 64.8 67.7 64.8 0.5 cryoSlug
```

The first line is a comment line. The second line has the specimen name, the core azimuth (a=) and plunge (b=) which are assumed to be the lab arrow azimuth and plunge (Orientation scheme #4)D. The third line is a header explaining the columns in the file.

Use **PMD_magic.py** to convert the file *ss0101a.pmd* in the directory 'PMD' in the 'PMD_magic' folder of the *Measurement_import* directory in the example *data_files* directory. These were taken at a location named 'Summit Springs' and have a naming convention of the type XXXX[YYY], where YYY is sample designation with Z characters from site XXX, or

```
$ PMD_magic.py -f ss0101a.pmd -loc "Summit Springs" -ncn 4-2 -spc 1 -mcd SO-MAG -F ss01
  results put in ./magic_measurements.txt
  sample orientations put in ./er_samples.txt
```

Because each file must be imported separately, you should use a different name for the output file for each input file (otherwise you will overwrite the default each time) and set the switch for sample file to append for subsequent imports:

```
$ PMD_magic.py -f ss0102a.pmd -loc "Summit Springs" -ncn 4-2 -spc 1 -mcd SO-MAG -F ss01
  sample information will be appended to ./er_samples.txt
  results put in ./magic_measurements.txt
  sample orientations put in ./er_samples.txt
```

After you finish importing all the data, combine the individual files together with *combine_magic.py* and look at them with, for example, *zeq_magic.py*.

sio_magic.py

[*sio_magic docs*]

The program **sio_magic.py** allows conversion of the SIO format magnetometer files to the MagIC common measurements format. It allows various experiment types so read the help message. The SIO format is a space delimited file:

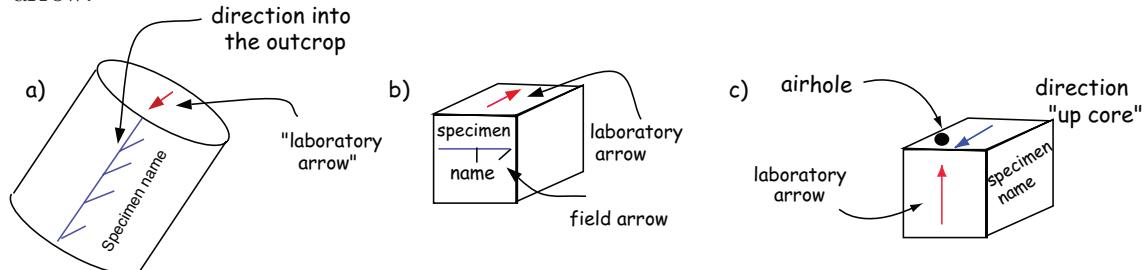
sc12b1	0.00	0.3	2.878E-2	185.0	9.3
sc12b1	5.00	0.3	2.864E-2	187.7	9.6

sc12b1	10.00	0.3	2.833E-2	185.5	10.0
sc12b1	15.00	0.2	2.771E-2	188.2	10.0
sc12b1	20.00	0.4	2.644E-2	187.6	10.1
sc12b1	30.00	0.2	2.182E-2	186.0	9.9
sc12b1	40.00	0.4	1.799E-2	185.3	9.9
sc12b1	50.00	0.2	1.570E-2	187.9	9.6
sc12b1	60.00	0.2	1.423E-2	185.6	10.0
sc12b1	80.00	0.1	1.275E-2	187.4	9.5

The columns are:

Specimen treatment intensity declination inclination optional_string

The treatment field is the temperature (in centigrade), the AF field (in mT), the impulse field strength, etc. For special experiments like IRM acquisition, the coil number of the popular ASC impulse magnetizer can be specified if the treatment steps are in volts. The position for anisotropy experiments or whether the treatment is “in-field” or in zero field also require special formatting. The units of the intensity field are in cgs and the directions are relative to the ‘lab arrow’ on the specimen. Here are some examples of commonly used specimens and conversions from field arrow to lab arrow.



As an example, we use data from Sbarboli et al. (2009) done on a set of samples from the location “Socorro”, including AF, thermal, and thellier experimental data. These were saved in *sio_af_example.dat*, *sio_thermal_example.dat*, and *sio_thellier_example.dat* respectively. The lab field for the thellier experiment was $25 \mu\text{T}$ and was applied along the specimen’s Z axis ($\phi=0, \theta=90$).] Convert the example files into *magic_measurement* formatted files with names like *af_measurements.txt*, etc. Then combine them together with *combine_magic.py*:

Note: all of these should actually be on ONE line:

```
$ sio_magic.py -f sio_af_example.dat -F af_measurements.txt
-LP AF -spc 1 -loc Socorro
```

```
averaging: records 11 13
averaging: records 14 16
averaging: records 17 19
averaging: records 20 22
sc12b1 started with 22 ending with 14
Averaged replicate measurements
results put in af_measurements.txt
```

```
$ sio_magic.py -f sio_thermal_example.dat -F thermal_measurements.txt \
-LP T -spc 1 -loc Socorro
averaging: records 6 7
sc12b2 started with 23 ending with 22
Averaged replicate measurements
results put in thermal_measurements.txt
```

```
$ sio_magic.py -f sio_thellier_example.dat -F thellier_measurements.txt \
-LP T -spc 1 -loc Socorro -dc 25 0 90
averaging: records 10 11
sc12b2 started with 56 ending with 55
Averaged replicate measurements
results put in thellier_measurements.txt
```

```
$ combine_magic.py -F magic_measurements.txt -f thellier_measurements.txt \
thermal_measurements.txt af_measurements.txt

File ./thermal_measurements.txt read in with 22 records
File ./thellier_measurements.txt read in with 55 records
File ./af_measurements.txt read in with 14 records
All records stored in ./magic_measurements.txt
```

The data in these files can be plotted and interpreted with dmag_magic.py, zeq_magic.py, or thellier_magic.py depending on the experiment.

Note that there are more examples of data file formats and import schemes in the sections on anisotropy of anhysteretic and thermal rema-

nences.

SUFAR4-asc_magic.py

[Essentials Chapter 13]; [MagIC Database] [SUFAR4-asc_magic docs]

The Agico Kappabridge instrument comes with the SUFAR program which makes the measurements and saves the data in a txt file like that in *SUFAR4-asc_magic_example.txt* in the *SUFAR4-asc_magic* directory. These data were measured on a KLY4S instrument with a spinning mode. Import them into the MagIC format:

```
%SUFAR4-asc_magic.py -f SUFAR4-asc_magic_example.txt -loc U1356A -spc 0 -ncn 5
anisotropy tensors put in ./rmag_anisotropy.txt
bulk measurements put in ./magic_measurements.txt
specimen info put in ./er_specimens.txt
sample info put in ./er_samples.txt
site info put in ./er_sites.txt
```

You can now import your data into the Magic Console and complete data entries for example the site locations, lithologies, etc. plotting can be done with *aniso_magic.py*

TDT_magic.py

[Essentials Chapter 10] and [MagIC] [TDT_magic docs]

This program imports the default data format for the ThellierTool Program of Leonhardt et al. (2004). After importing, the data can be viewed with **thellier_magic.py**.

The file format of the ThellierTool .tdt format is:

```
Thellier-tdt
50.12 0 0 0 0
2396D 0.00 1821.50 4.6 49.4
2396D 200.00 1467.5 7.4 44.5
2396D 200.11 1808.3 4.3 34.4
2396D 200.13 1421.89 6.1 46
2396D 230.00 1317.69 6.9 45.3
2396D 230.11 1711.2 4.3 32.9
2396D 260.00 1150.89 8.4 44.7
2396D 200.12 1475.92 4.3 34.7
...
```

The first two lines are headers. The first column of the second line is the applied field in μT . The rest of this line is azimuth and plunge of the fiducial line and dip direction and dip of the bedding plane. The data columns are: specimen, treatment, intensity, declination and inclination. the intensity is the magnetization in 10^{-3} A/m . The treatment is of the form XXX.YY where XXX is the temperature and YY is 00, 11, 12, 13, 14 OR 0, 1, 2, 3, 4 where 0 is the NRM step, 11/1 is the pTRM acquisition step, 12/2 is the pTRM check step and 13/3 is the pTRM tail check. 14/4 is the additivity check.

Use the program **TDT_magic.py** to import the ThellierTool tdt formatted file *TDT_magic_example.dat* into the MagIC format. The field was $52.12 \mu\text{T}$ applied along the 0,0 direction.

```
$ TDT_magic.py -f tdt_magic_example.dat -loc TEST -dc 50.12 0 0
results put in magic_measurements.txt
```

5.2.67 measurements_normalize.py

[MagIC Database] [measurements_normalize docs]

This program takes specimen weights or volumes from an *er_specimen.txt* formatted file and normalizes the magnetic moment data to make magnetizations. Weights must be in kilograms and volumes in m^3 .

Use the program **measurements_normalize.py** to generate weight normalized magnetizations for the data in the file *magic_measurements.txt* in the —it *measurements_normalize* directory. Use the specimen weights in the file *specimen_weights.txt*.

```
$ magic_select.py -f magic_measurements.txt \
    -key magic_method_codes LP-IRM has -F irm_measurements.txt
205 records written to ./irm_measurements.txt
$ measurements_normalize.py -f irm_measurements.txt \
    -fsp specimen_weights.txt -F irm_norm_measurements.txt
Data saved in ./irm_norm_measurements.txt
```

5.2.68 mk_redo.py

MagIC [mk_redo docs]

The programs *zeq_magic.py* and *thellier_magic.py* as well as the two GUIs Demag GUI and Thellier GUI make *pmag-specimen* formatted files

which can be used for further data reduction either by plotting or contributing to site means, etc. Sometimes it is useful to redo the calculation, using anisotropy corrections or a change in coordinate systems, etc. The re-doing of these specimen level calculations is handled by, for example `zeq_magic_redo.py` or `thellier_magic_redo.py`. These programs use *magic_measurements* formatted files and perform calculations as dictated by a “redo” file which has the specimen name, bounds for calculation and, in the case of the demagnetization data interpretation, the type of calculation desired (best-fit lines with directional estimation magic method code:DE-BFL, best-fit planes with those with magic method code DE-BFP, etc.).

Make “redo” files from the existing *pmag-specimen* formatted file in the data files downloaded from the MagIC website as in **download_magic.py** and examine them as follows:

```
$ mk_redo.py
$ cat zeq_redo
sr01a1 DE-BFL 473 823 A
sr01a2 DE-BFL 473 848 A
sr01c2 DE-BFL 473 823 A
sr01d1 DE-BFL 373 798 A
.....
$ cat thellier_redo
sr01a1 573 823
sr01a2 573 848
sr01c2 673 823
sr01d1 373 823

.....
```

Note that the temperature steps are in kelvin and the AF demagnetization steps are in Tesla as required in the MagIC data base.

5.2.69 nrm_specimens_magic.py

MagIC [nrm_specimens_magic docs]

After making NRM measurements, it is frequently useful to look at the directions in equal area projection to get a “quick look” at the results before proceeding to step wise demagnetization. The data in the *magic_measurements* files are usually in specimen coordinates - not geographic, so we need a way to rotate the data into geographic and or stratigraphic coordinates and save them in a *pmag-specimens* formatted file for

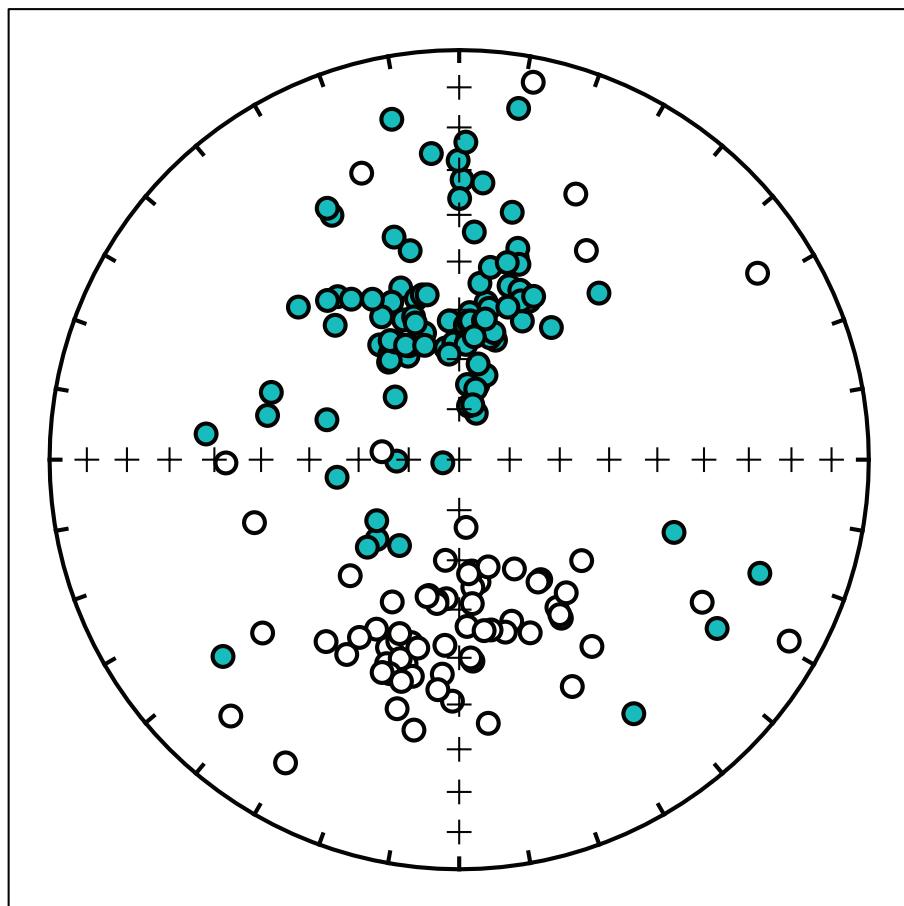
plotting with **eqarea_magic.py**. The program **nrm_specimens_magic.py** will do this for you.

Get into the directory you made for the **download_magic.py** example. Use **nrm_specimens_magic.py** to convert the NRM measurements in *magic_measurements.txt* to geographic coordinates saved in a file named *nrm_specimens.txt*. The orientation data are in the file *er_samples.txt*. Then plot the specimen directions for the entire study using **eqarea_magic.py**:

```
$ nrm_specimens_magic.py -crd g  
er_samples.txt  read in with 271 records  
Data saved in nrm_specimens.txt  
  
$ eqarea_magic.py -f nrm_specimens.txt  
177 records read from ./nrm_specimens.txt  
All  
sr01a1 SO-SUN    324.1    66.0  
sr01a2 SO-SUN    325.3    62.1  
sr01c2 SO-SUN    344.7    63.8  
sr01d1 SO-CMD-NORTH 327.8    64.5  
sr01e2 SO-SUN    333.7    67.0  
...
```

The first command created a file *nrm_specimens.txt* and the second created an equal area projection of the NRM directions in geographic coordinates which should look like this:

All



5.2.70 orientation_magic.py

[Essentials Chapter 9] and [Preparing for MagIC] [orientation_magic docs]

Try to import the file *orientation_example.txt* into the *er_samples.txt* and *er_sites.txt* files using **orientation_magic.py**. Click here for details about the *orient.txt* file format. It has field information for a few sites. The samples were oriented with a Pomeroy orientation device (the default) and it is desirable to calculate the magnetic declination from the IGRF at the time of sampling (also the default). Sample names follow the rule that the sample is designated by a letter at the end of the site name (convention #1 - which is the default). So we do this by:

```
orientation_magic.py -f orient_example.txt
```

```
saving data...
Data saved in ./er_samples.txt and ./er_sites.txt
```

5.2.71 parse_measurements.py

This program reads in the *magic_measurements.txt* file and creates an *er_specimens.txt* file. The specimen volumes and/or weights can then be put in columns labeled **specimen_volume** and **specimen_weight** respectively. Volumes must be in m³ and weights in kg. (Yes you can do the math...).

Try this out on the *magic_measurements.txt* file created in the *irmaq_magic.py* example. Pretend you have a bunch of specimen weights you want to use to normalize the NRM with the program *measurements_normalize.py*.

```
$ parse_measurements.py
site record in er_sites table not found for: 318-U1359A-002H-1-W-109
site record in er_sites table not found for: 318-U1359A-002H-2-W-135
site record in er_sites table not found for: 318-U1359A-002H-3-W-45
site record in er_sites table not found for: 318-U1359A-002H-4-W-65
....
```

The program appears a bit flustered because you have no *er_sites.txt* file in this directory. If you DID, you would overwrite whatever site name was in that file onto the specimen table. This allows you to carry the changes in that table through to the specimen table (see *orientation_magic.py*.)

5.2.72 pca.py

[Essentials Chapter 11] [pca docs]

This program calculates best-fit lines, planes or Fisher averages through selected treatment steps. The file format is a simple space delimited file with specimen name, treatment step, intensity, declination and inclination. Calculate the best-fit line through the first ten treatment steps in data file *zeq_example.txt*:

```
$ pca.py -dir L 1 10 -f zeq_example.dat
eba24a DE-BFL
0 0.00 339.9 57.9 9.2830e-05
1 2.50 325.7 49.1 7.5820e-05
...
eba24a DE-BFL 10      2.50  70.00     8.8   334.9     51.5
```

According to the help message, this is: specimen name, calculation type, N, beg, end, MAD, declination and inclination. The calculation type is the MagIC method code for best-fit lines (see Essentials Appendix ??.)

5.2.73 plotXY.py

[plotXY docs]

This program makes a simple XY plot from any arbitrary input file. You can specify which columns are X and Y, bounds on the columns, symbol color and size, axis labels and other options.

```
$ plotXY.py -f plotXY_example.txt
```

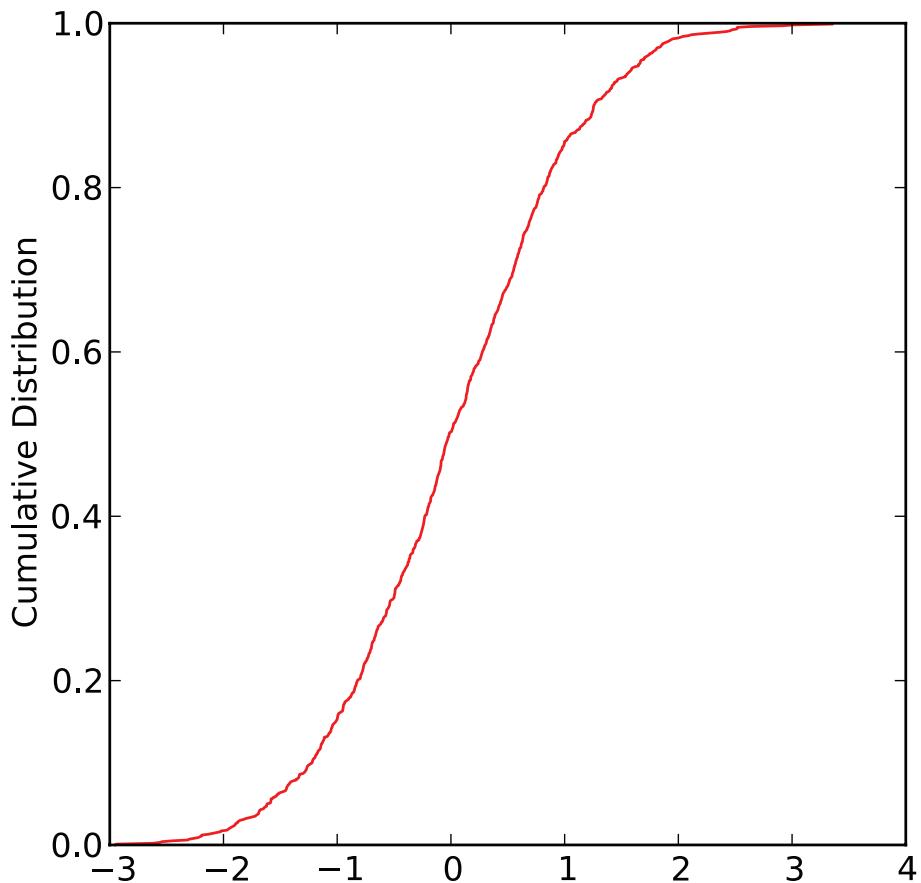
5.2.74 plot_cdf.py

[plot_cdf docs]

This program plots cumulative distribution functions of a single column of input data. Use as an example, a normally distributed set of 1000 data points generated by gaussian.py. Use the defaults of zero mean with a standard deviation of 1.

```
$ gaussian.py -n 1000 > gaussian.out
$ plot_cdf.py -f gaussian.out
S[a]ve plot, <Return> to quit a
1 saved in CDF_.svg
```

which should have generated a plot something like this:



5.2.75 plot_magic_keys.py

MagIC [plot_magic_keys docs]

This program will plot any column in a specified MagIC formatted file against any other column in the same file.

5.2.76 plot_mapPTS.py

high resolution instructions [plot_mapPTS docs]

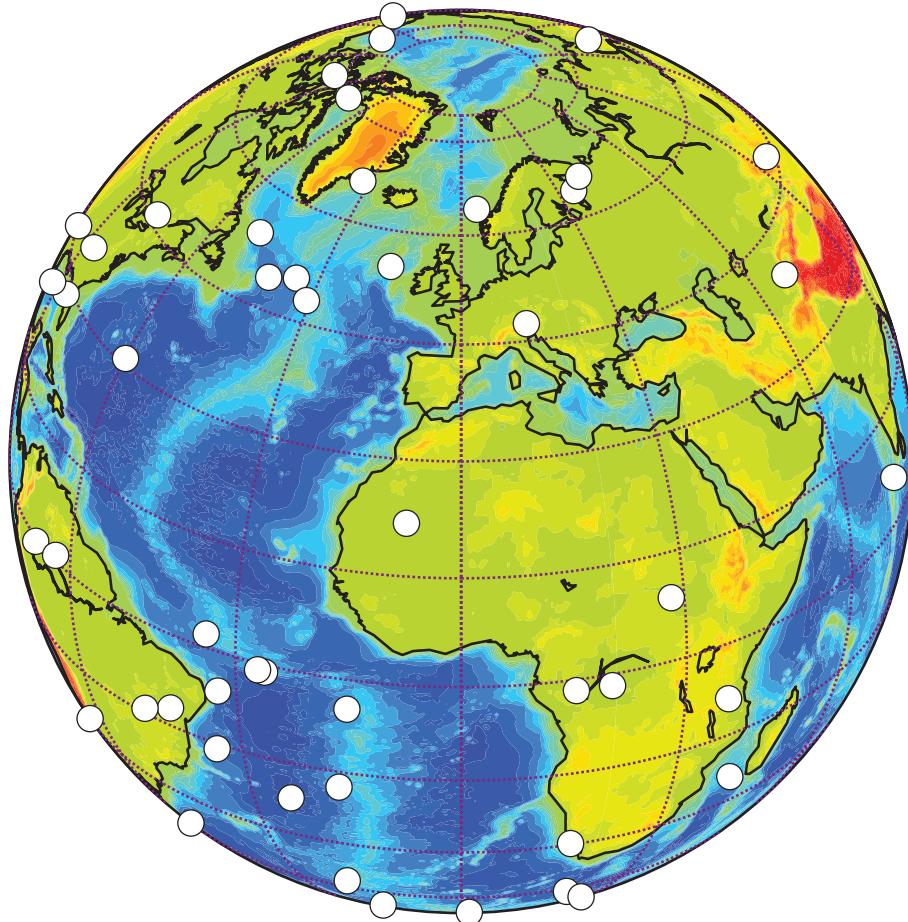
NOTE: This program only works if you have installed basemap (full version of Canopy Python as opposed to the free version.) It may not work with free versions. **plot_mapPTS.py** will generate a simple map of the data points in a file (lon lat) on the desired projection. If you want to use high resolution or the etopo20 meshgrid (-etp option), You must install the

etopo20 data files and can use `install_etopo.py` for that. There are many options, so check the documentation (`-h` option) for details.

Draw a set of 200 uniformly distributed points on the globe with the program `uniform.py`. Plot these on an orthographic projection with the viewing point at a longitude of 0 and a latitude of 30°N. If you have installed the high resolution data sets, use the `-etp` option to plot the topographic mesh. Plot the points as large (size = 10) white dots. Also note that for some reason the `.svg` output does not place nicely with illustrator.

```
$ uniform.py -n 200 >uniform.out
$ plot_mapPTS.py -f uniform.out -prj ortho -eye 30 0 -etp -sym wo 10
please wait to draw points
S[a]ve to save plot, Return to quit: a
1 saved in Map PTS.pdf
```

which should produce a plot similar to this:



5.2.77 plotdi_a.py

[Essentials Chapter 11] [plotdi_a docs]

Place the following declination, inclination α_{95} data in a space delimited file called

plotdi_a_example.dat.

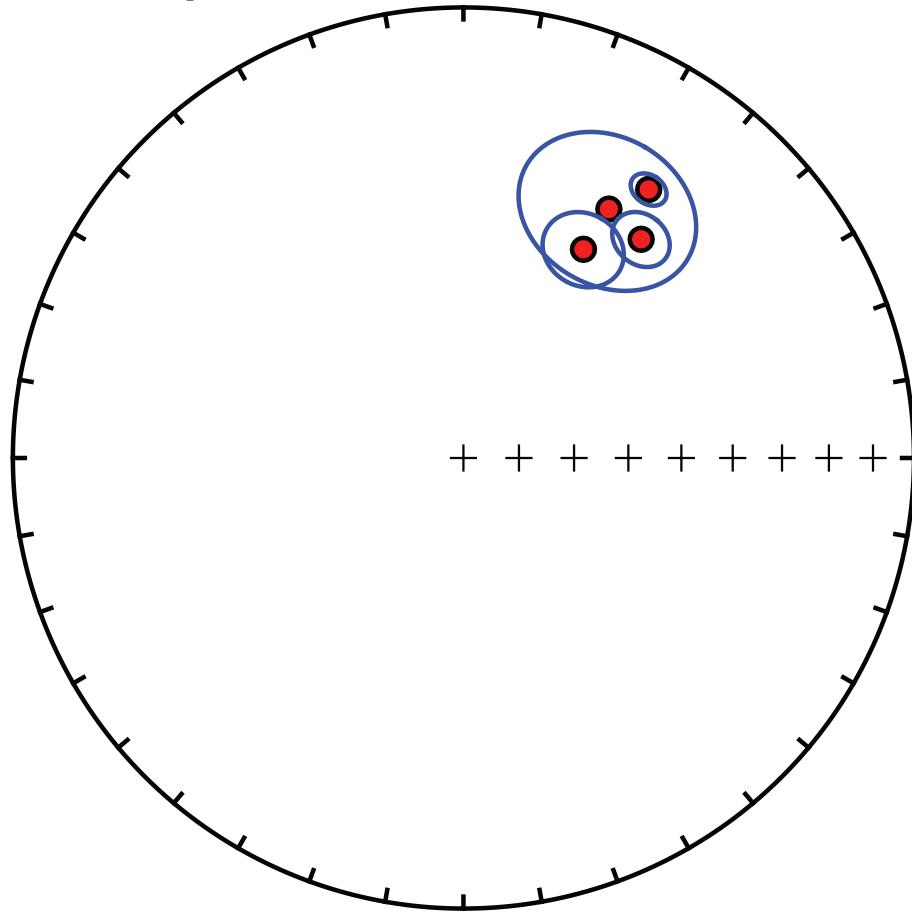
Dec	Inc	α_{95}
39.1	37.5	5.0
30.3	36.2	15
29.9	45.6	7
34.6	28.4	3

Make a plot of these data using **plotdi_a.py**:

```
$ plotdi_a.py -f plotdi_a_example.dat
```

```
S[a]ve to save plot, [q]uit, Return to continue: a
1 saved in eq.svg
```

which makes the plot:



5.2.78 pmag_results_extract.py

[:MagIC] [pmag_results_extract docs]

This program extracts a tab delimited txt file from a *pmag-results* formatted file. This allows you to publish data tables that have identical data to the data uploaded into the MagIC database. Try this out in the directory created for the **download_magic.py** example:

```
$ pmag_results_extract.py -f pmag_results.txt
data saved in: ./Directions.txt ./Intensities.txt ./SiteNfo.txt
```

This creates tab delimited files that can be incorporated into a paper, for example. You can also export the information in LaTeX format if you prefer.

5.2.79 pt_rot.py

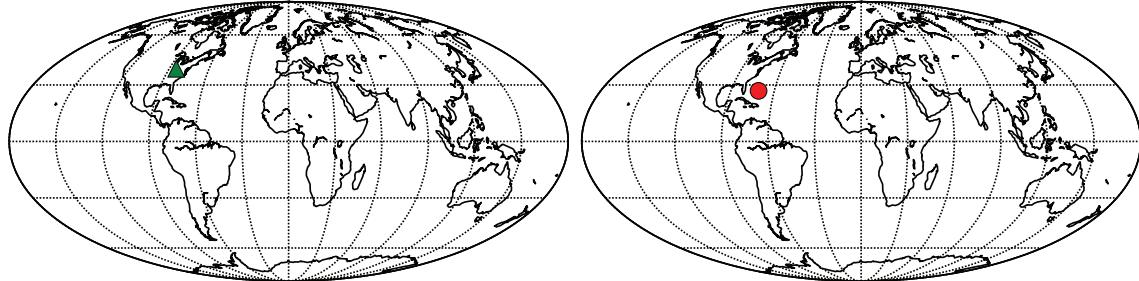
[Essentials Chapter 16] [pt_rot docs]

This program reads in a file with location, age and destination plate and rotates the data into the destination plate coordinates using the rotations and methods in Essentials Appendix A.3.5. Alternatively, you can supply your own rotation parameters with the -ff option.

First, save the location of Cincinnati (39.1 latitude, -84.7 longitude) in a file called *pt_rot.input* using either the UNIX **cat** function or your favorite text editor. Save the data as a lon/lat pair separated by a space. Then use the program **pt_rot.py** to rotate Cincinnati to (South) African (saf) coordinates at 80 Ma. Plot both points using **plot_mapPTS.py**. You should save the lon, lat, plate, age, destination_plate information in a file called *pt_rot_example.dat* in the following:

```
$ awk '{print $1,$2}' pt_rot.input > lon_lat
$ -prj moll -f lon_lat -sym g^ 10 -R -B -eye 0 0
please wait to draw points
S[al]ve to save plot, Return to quit: a
1 saved in Map PTS.pdf
$ pt_rot.py -f pt_rot.input pt_rot_example.dat
299.763594614 34.6088989286
$ pt_rot.py -f pt_rot_example.dat >pt_rot.out
$ plot_mapPTS.py -f pt_rot.out -sym ro 10
please wait to draw points
S[al]ve to save plot, Return to quit: a
1 saved in Map PTS.pdf
```

The two plots will look like these:

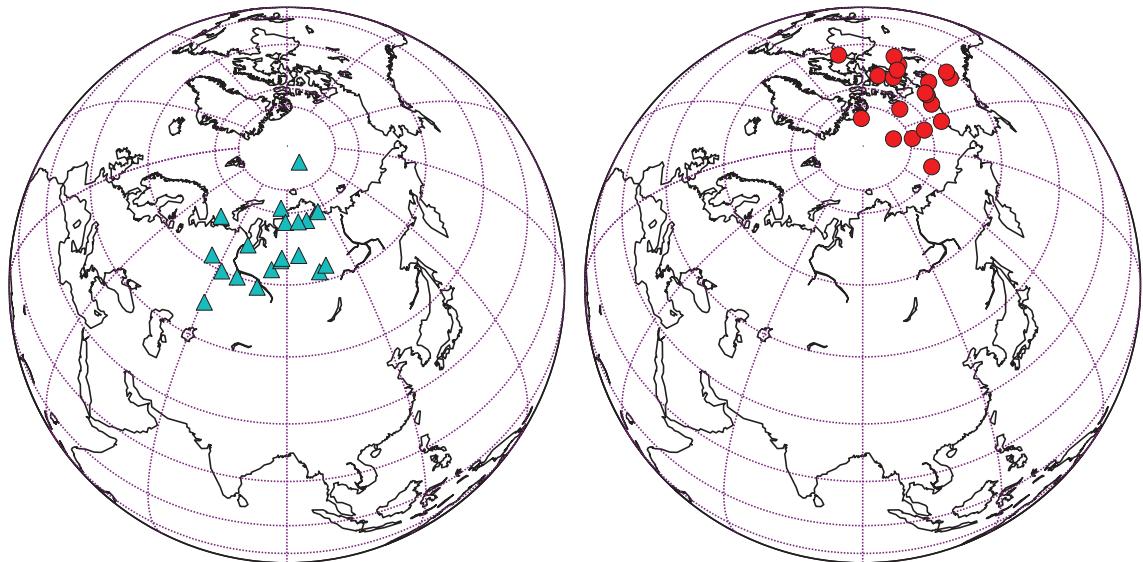


Now, use the program to rotate a selection of North American poles from 180-200 Ma (in the file *nam_180-200.txt* in the *pt_rot* directory) to Pangea A coordinates (finite rotation pole and angle in *nam_panA.frp*). Note that *plot_mapPTS.py* reads in longitude/latitude pairs, while *pt_rot.py* reads in latitude longitude pairs.

```
$ plot_mapPTS.py -f nam_180-200.txt -prj ortho -eye 60 90 -sym c^ 10
please wait to draw points
S[a]ve to save plot, Return to quit: a
1 saved in Map_PTS.pdf

$ pt_rot.py -ff nam_180-200.txt nam_panA.frp
165.005966833 75.1055653383
272.368103052 83.1542552681
281.233199772 63.3738811186
260.36973769 70.7986591555
250.91392318 70.3067026787
251.438099128 65.9369002914
255.371917029 63.4115373574
204.92422073 71.7944043036
.....
$ pt_rot.py -ff nam_180-200.txt nam_panA.frp > pt_rot_panA.out
$ plot_mapPTS.py -f pt_rot_panA.out -prj ortho -eye 60 90 -sym ro 10
please wait to draw points
S[a]ve to save plot, Return to quit: a
1 saved in Map_PTS.pdf
```

These plots should look like this:



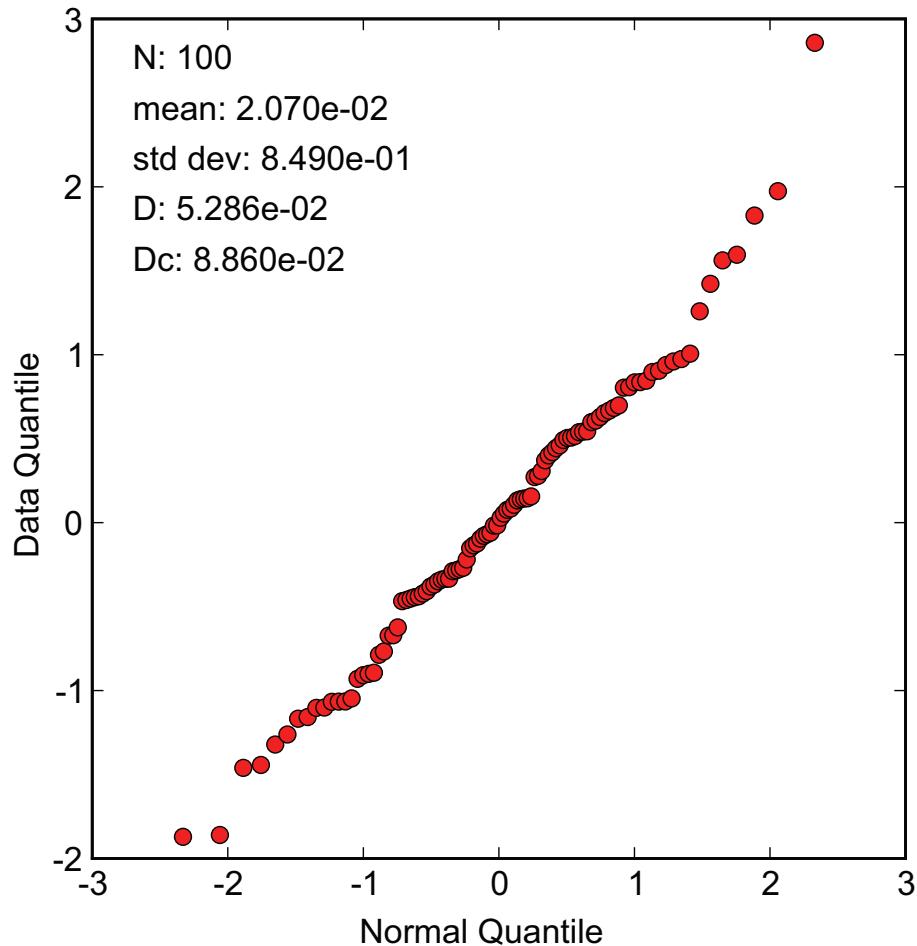
5.2.80 qqplot.py

[Essentials Appendix B.1.5] [qqplot docs]

Makes a quantile-quantile plot of the input data file against a normal distribution. The plot has the mean, standard deviation and the D statistic as well as the D_c statistic expected from a normal distribution. Use **qqplot.py** to test whether the data generated with **gaussian.py** is in fact normally distributed. (It will be 95% of the time!).

```
$ gaussian.py -F gauss.out
$ qqplot.py -f gauss.out
mean,sigma, d, Dc
0.02069909 0.849042146783 0.0528626896977 0.0886
S[a]ve to save plot, [q]uit without saving: a
1 saved in qq.svg
```

which generates this plot:



5.2.81 quick_hyst.py

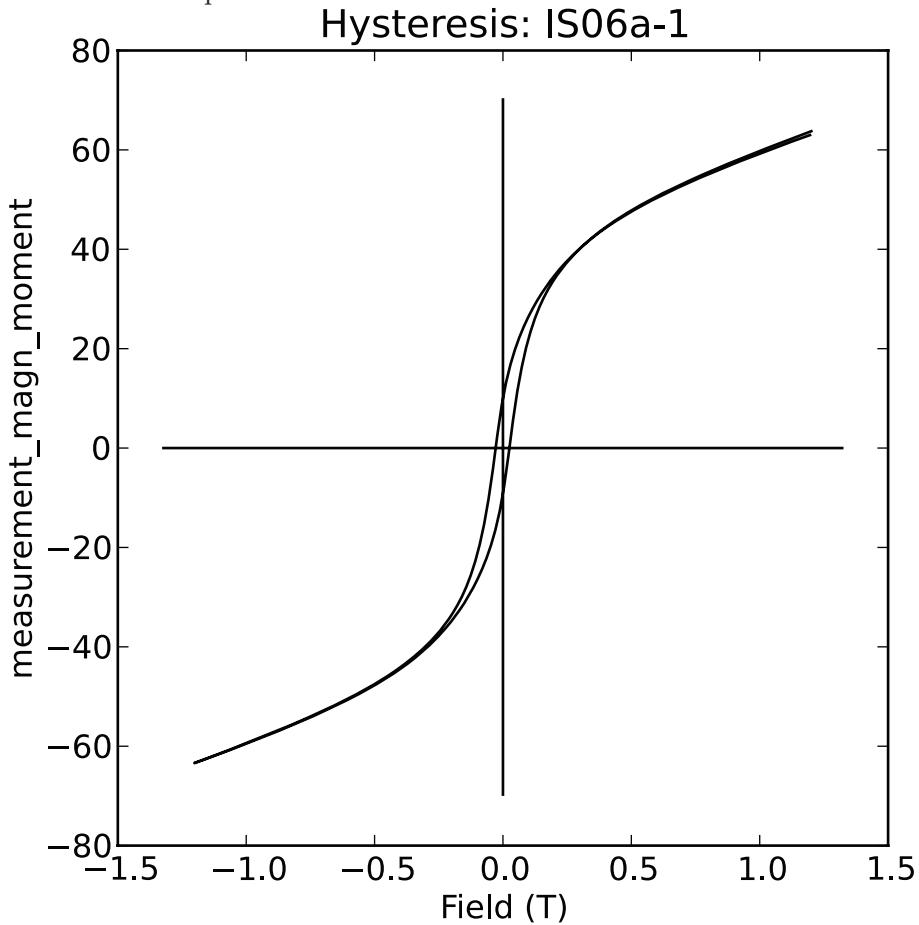
[Essentials Chapter 5] and [MagIC Database] [quick_hyst docs]

`hysteresis_magic.py` makes plots of hysteresis loops and calculates the main hysteresis parameters. For a quick look with no interpretation, you can use **quick_hyst.py**. Try it out on the data file `hysteresis_magic_example.dat` in the `hysteresis_magic` directory.

```
$ quick_hyst.py -f hysteresis_magic_example.dat -fmt svg
IS06a-1 1 out of  8
working on t: 273
S[a]ve plots, [s]pecimen name, [q]uit, <return> to continue
a
```

```
1 saved in LO:_SI:_IS06_SA:_IS06a_SP:_IS06a-1_TY:_hyst_.svg
IS06a-1 1 out of 8
working on t: 273
S[a]ve plots, [s]pecimen name, [q]uit, <return> to continue
q
Good bye
```

which makes a plot like this:



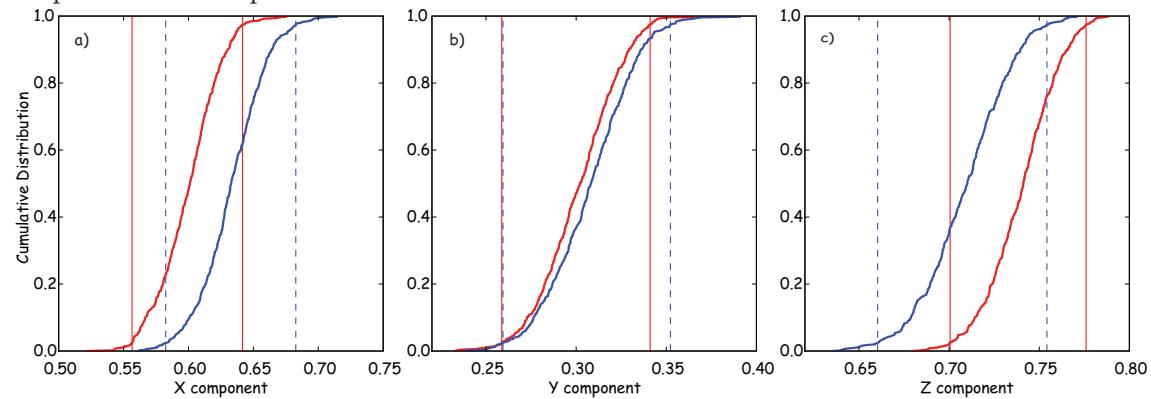
5.2.82 revtest.py

[Essentials Chapter 12] [revtest docs]

Use the Tauxe et al., (2010) reversals test implemented in **revtest.py** to test whether the two modes in the data set *revtest_example.txt* are antipodal or not:

```
$ revtest.py -f revtest_example.txt
doing first mode, be patient
doing second mode, be patient
s[a]ve plots, [q]uit: a
2 saved in REV_Y.svg
1 saved in REV_X.svg
3 saved in REV_Z.svg
```

which produces these plots:



Because the 95% confidence bounds for each component overlap each other, the two directions are not significantly different.

5.2.83 revtest_magic.py

[Essentials Chapter 12] and MagIC [revtest_magic docs]

Same as revtest.py but for *pmag_sites* MagIC formatted files. Try it out on the data file *revtest_sites.txt*. Then try using *customize_criteria.py* to change or create a *pmag_criteria.txt* file that fits your needs and redo the reversals test using only the selected sites.

```
revtest_magic.py -f revtest_magic_example.txt
doing first mode, be patient
doing second mode, be patient
s[a]ve plots, [q]uit: q
$ revtest_magic.py -f revtest_sites.txt -exc
```

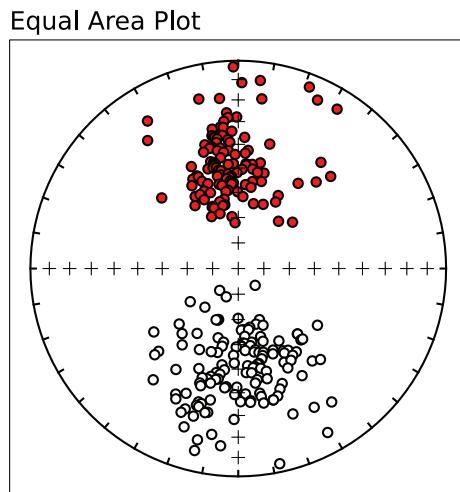
5.2.84 revtest_MM1990.py

[revtest_MM1990 docs]

This program tests whether two sets of observations (one with normal and one with reverse polarity) could have been drawn from distributions that are 180° apart using the McFadden and McElhinny (1990) implementation of the Watson (1983) V statistic test for a common mean. The implementation of the V statistic test in this program is the same as in WatsonsV.py. Use **revtest_MM1990.py** to perform a reversal test on data from the Ao et al., 2013 study of Early Pleistocene fluvio-lacustrine sediments of the Nihewan Basin of North China.

Lets plot the combined data set *Ao_etal2013_combined.txt* using eqarea.py:

```
$ eqarea.py -f Ao_etal2013_combined.txt
```



Conduct a reversal test between the normal directions *Ao_etal2013_norm.txt* and reversed directions *Ao_etal2013_rev.txt*:

```
$ MM1990_revtest.py -f Ao_etal2013_norm.txt -f2 Ao_etal2013_rev.txt
be patient, your computer is doing 5000 simulations...
```

Results of Watson V test:

Watson's V: 2.7

Critical value of V: 6.0

“Pass”: Since V is less than Vcrit, the null hypothesis that the

two populations are drawn from distributions that share a common mean direction (antipodal to one another) cannot be rejected.

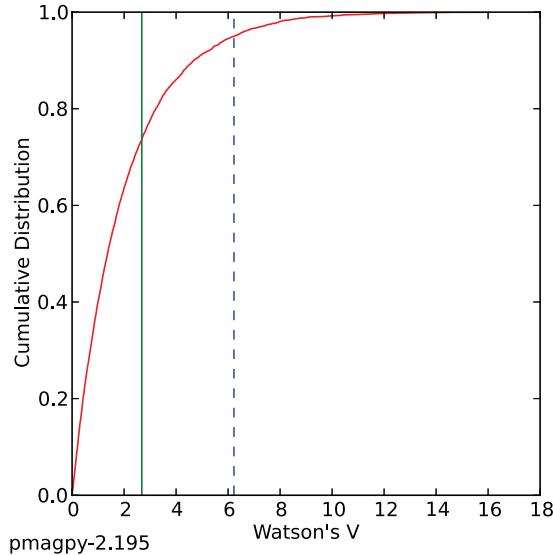
M&M1990 classification:

Angle between data set means: 2.9

Critical angle for M&M1990: 4.3

The McFadden and McElhinny (1990) classification for this test is: ‘A’

As with WatsonsV.py, this program produces a plot that displays the cumulative distribution (CDF) of the Watson V values resulting from the Monte Carlo simulation. In the plot below, the red line is the CDF, the green solid line is the value of the V statistic calculated for the two populations and the dashed blue line is the critical value for the V statistic. In this example, the data are consistent with the two directional groups sharing a common mean as evidenced by V (green solid line) being a lower value than the critical value of V (dashed blue line).



5.2.85 s_eigs.py

[Essentials Chapter 13] [s_eigs docs]

Convert the .s format data in *s_eigs-example.dat* to eigenvalues and eigenvectors:

```
$ s_eigs.py -f s_eigs_example.dat
0.33127186 239.53 44.70 0.33351338 126.62 21.47 0.33521473 19.03 37.54
0.33177859 281.12 6.18 0.33218277 169.79 73.43 0.33603862 12.82 15.32
0.33046979 283.57 27.30 0.33328307 118.37 61.91 0.33624712 16.75 6.13
...
```

5.2.86 s_geo.py

[Essentials Chapter 13] [s_geo docs]

Rotate the .s data into geographic coordinates using **s_geo.py**. The input format is the 6 tensor elements of s, followed by the azimuth and plunge of the X axis.

```
$ s_geo.py -f s_geo_example.dat
0.33412680 0.33282733 0.33304587 -0.00015289 0.00124843 0.00135721
0.33556300 0.33198264 0.33245432 0.00087259 0.00024141 0.00096166
0.33584908 0.33140627 0.33274469 0.00131845 0.00118816 0.00002986
...
```

5.2.87 s_hext.py

[Essentials Chapter 13] [s_hext docs]

Take the output from the **s_geo.py** example and calculate Hext statistics:

```
$ s_geo.py -f s_geo_example.dat | s_hext.py
F = 5.79 F12 = 3.55 F23 = 3.66
N = 8 sigma = 0.000641809950
0.33505      5.3    14.7    25.5   124.5    61.7    13.3    268.8    23.6
0.33334     124.5   61.7    25.1    268.8    23.6    25.5      5.3    14.7
0.33161     268.8   23.6    13.3      5.3    14.7    25.1    124.5    61.7
```

5.2.88 s_tilt.py

[Essentials Chapter 13] [s_tilt docs]

Rotate the .s data saved in *s_tilt_example.dat* into stratigraphic coordinates:

```
$ s_tilt.py -f s_tilt_example.dat
0.33455709 0.33192658 0.33351630 -0.00043562 0.00092778 0.00105006
```

```

0.33585501 0.33191565 0.33222935 0.00055959 -0.00005316 0.00064731
0.33586669 0.33084923 0.33328408 0.00142267 0.00013233 0.00009202
0.33488664 0.33138493 0.33372843 -0.00056597 -0.00039086 0.00004873
.
.
```

5.2.89 s_magic.py

[MagIC] [MagIC Database] [s_magic docs]

Import .s format file output from the `s_tilt.py` example into an `rmag_anisotropy` formatted file. Files of the `rmag_anisotropy` format can be plotted with `aniso_magic.py`. To see how this works, use the program `s_magic.py` as follows:

```

$ s_tilt.py -f s_tilt_example.dat >s_magic_example.dat
$ s_magic.py -f s_magic_example.dat
data saved in ./rmag_anisotropy.txt
```

This creates the output file `rmag_anisotropy.txt` by default, which can be plotted with the program `aniso_magic.py`.

5.2.90 scalc.py

[Essentials Chapter 14] [scalc docs]

Calculate the S scatter statistic for a set of VGPs saved in `scalc_example.txt`. Repeat using a Vandamme (Vandamme et al., 1994) variable cutoff. Then get the bootstrap bounds on the calculation.

```

$ scalc.py -f scalc_example.txt
99      19.5      90.0
$ scalc.py -f scalc_example.txt -v
89      15.2      32.3
$ scalc.py -f scalc_example.txt -v -b
89      15.2      13.3      16.8      32.3
```

Using no cutoff, the VGP scatter was 19.5° . The Vandamme co-latitude cutoff was 32.3° which threw out 6 points and gave a scatter of 15.2° .

5.2.91 scalc_magic.py

[Essentials Chapter 14] [scalc_magic docs]

This is the same as **scalc.py** but works on *pmag_results* formatted files. Try it out on the *pmag_results.txt* file in the directory created for the **download_magic.py** example. Use a VGP co-latitude cutoff of 30°.

```
$ scalc_magic.py -f pmag_results.txt -c 30
13    17.8    30.0
```

5.2.92 site_edit_magic.py

[site_edit_magic docs]

There are frequently outlier directions when looking at data at the site level. Some paleomagnetists throw out the entire site, while some arbitrarily discard individual samples, assuming that the orientations were ‘bad’. Lawrence et al. (2009) suggested a different approach in which common causes of misorientation are specifically tested. For example, if the arrow indicating drill direction (see orientation conventions) was drawn the wrong way on the sample in the field, the direction would be off in a predictable way. Similarly (and more commonly) extraneous marks on the sample were used instead of the correct brass mark, the directions will fall along a small circle which passes through the correct direction. The program **site_edit_magic.py** plots data by site on an equal area projection, allows the user to select a particular specimen direction and plots the various pathological behaviors expected from common misorientations. If the stray directions can reasonably be assigned to a particular cause, then that sample orientation can be marked as ‘bad’ with a note as to the reason for exclusion and the directions from that sample can be excluded from the site mean, and the reason can be documented in the MagIC database.

Try this out using the data downloaded in the **download_magic.py** example.

```
$ site_edit_magic.py
....
sr11
specimen, dec, inc, n_meas/MAD, | method codes
sr11a1: 340.6    74.1 8 / 0.9 | LP-DIR-AF:DE-BFL
sr11b1: 353.9    70.3 10 / 2.1 | LP-DIR-AF:DE-BFL
sr11c1: 342.6    69.4 8 / 1.3 | LP-DIR-AF:DE-BFL
```

```

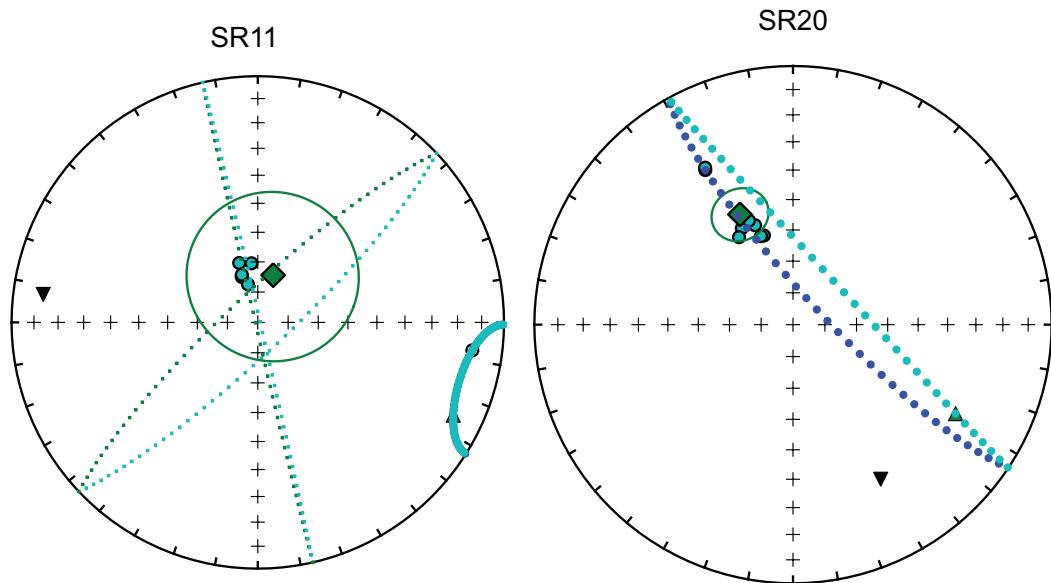
sr11e2: 341.5    73.4 8 / 0.9 | LP-DIR-AF:DE-BFL
sr11f1: 136.6     9.4 14 / 3.5 | LP-DIR-T:DE-BFP
sr11g2: 345.5    77.0 8 / 0.8 | LP-DIR-AF:DE-BFL
sr11i1: 77.1      0.8 12 / 3.5 | LP-DIR-AF:DE-BFP
sr11j3: 97.4     -13.2 8 / 11.8 | LP-DIR-AF:DE-BFL

Site lines planes  kappa   a95   dec   inc
sr11 6 2         5       28.4     18.0     73.6  6.7445
s[a]ve plot, [q]uit, [e]dit specimens, [p]revious site, <return> to continue:
e
Enter name of specimen to check: sr11j3
Triangle: wrong arrow for drill direction.
Delta: wrong end of compass.
Small circle: wrong mark on sample. [cyan upper hemisphere]
Mark this sample as bad? y/[n] n
Mark another sample, this site? y/[n] n
.....
sr20
no orientation data for sr20j
specimen, dec, inc, n_meas/MAD,| method codes
sr20c1: 339.1    56.2 9 / 2.1 | LP-DIR-T:DE-BFL
sr20d2: 341.9     60.3 9 / 1.7 | LP-DIR-AF:DE-BFL
sr20e1: 332.1    55.3 10 / 1.0 | LP-DIR-AF:DE-BFL
sr20f1: 337.1     54.0 9 / 3.7 | LP-DIR-T:DE-BFL
sr20g1: 340.1     60.2 9 / 1.6 | LP-DIR-T:DE-BFL
sr20i1: 330.4     31.9 11 / 0.6 | LP-DIR-AF:DE-BFL
sr20i2: 330.7     31.1 9 / 2.3 | LP-DIR-T:DE-BFL

Site lines planes  kappa   a95   dec   inc
sr20 7 0         38      9.9     335.1    50.0  6.8434
s[a]ve plot, [q]uit, [e]dit specimens, [p]revious site, <return> to continue:
e
Enter name of specimen to check: sr20i1
Triangle: wrong arrow for drill direction.
Delta: wrong end of compass.
Small circle: wrong mark on sample. [cyan upper hemisphere]
Mark this sample as bad? y/[n] y
Reason: [1] broke, [2] wrong drill direction, [3] wrong compass direction,
[4] bad mark, [5] displaced block [6] other 2
Mark another sample, this site? y/[n] n

```

Compare behaviors for sr11, sample sr11XXX and sr20, sample sr20i:



The latter plausibly fits the “wrong mark” hypothesis, while the former does not fit any of the common pathologies. The sample orientation in the *er_samples.txt* file has a note that it is ‘bad’ and will be ignored by the PmagPy programs when calculating site means.

5.2.93 specimens_results_magic.py

MagIC [specimens_results_magic docs]

Starting from the magnetometer output files, paleomagnetists interpret the data in terms of vectors, using software like *zeq_magic.py* or *thellier_magic.py*. The interpretations from these programs are stored in *pmag-specimen* formatted files. Once a *pmag-specimens* format file has been created, the data are usually averaged by sample and/or by site and converted into V[A]DMs and/or VGPs and put in a *pmag-results* formatted file along with the location and age information that are available. Data must be selected or rejected according to some criteria at each level (for example, the specimen MAD direction must be less than some value or the site κ must be greater than some value). This onerous task can be accomplished using the program **specimens_results_magic.py**. This program has many optional features,

so the reader is encouraged just to look at the documentation.

Test it out by using the data files created in the `site_edit_magic.py` example. Block the interpretation of some of the samples owing to ‘bad’ orientation. Change the selection criteria using `customize_criteria.py`. Then generate a new `pmag_specimen.txt` file using `mk_redo.py`, `zeq_magic_redo.py` and `combine_magic.py`. Then do the averaging by site with `specimens_results_magic.py`. The age bounds of the data are 0-5 Ma (-age 0 5 Ma). Use the existing (or modified) criteria (-exc option). There are some paleointensity data, so use the current site latitude for the VADM calculation (-lat option). Calculate the data in the geographic coordinate system (-crd g). Then extract the data into tab delimited tables using `pmag_results_extract.py`

```
$ mk_redo.py
$ zeq_magic_redo.py -crd g
Processing 173 specimens - please wait
Recalculated specimen data stored in ./zeq_specimens.txt
$ combine_magic.py -F pmag_specimens.txt -f zeq_specimens.txt thellier_specimens
File ./zeq_specimens.txt read in with 173 records
File ./thellier_specimens.txt read in with 50 records
All records stored in ./pmag_specimens.txt
$ specimens_results_magic.py -age 0 5 Ma -exc -lat -crd g
Acceptance criteria read in from pmag_criteria.txt

Pmag Criteria stored in pmag_criteria.txt

sites written to pmag_sites.txt
results written to pmag_results.txt
$ pmag_results_extract.py -fa er_ages.txt
data saved in: ./Directions.txt ./Intensities.txt ./SiteNfo.txt
```

Note that this procedure is more or less automated in Pmag GUI.

5.2.94 stats.py

[Essentials Chapter 11] [stats docs]

Calculates gaussian statistics for sets of data. Calculate the mean of the data generated in the `gaussian.py` example and saved in `gauss.out`:

```
$ stats.py -f gauss.out
100 10.12243251 1012.243251 2.79670530387 27.6287868663
```

which according to the help message is:

```
N, mean, sum, sigma, (%) , stderr, 95% conf.
where sigma is the standard deviation
where % is sigma as percentage of the mean
stderr is the standard error and
95% conf.= 1.96*sigma/sqrt(N)
```

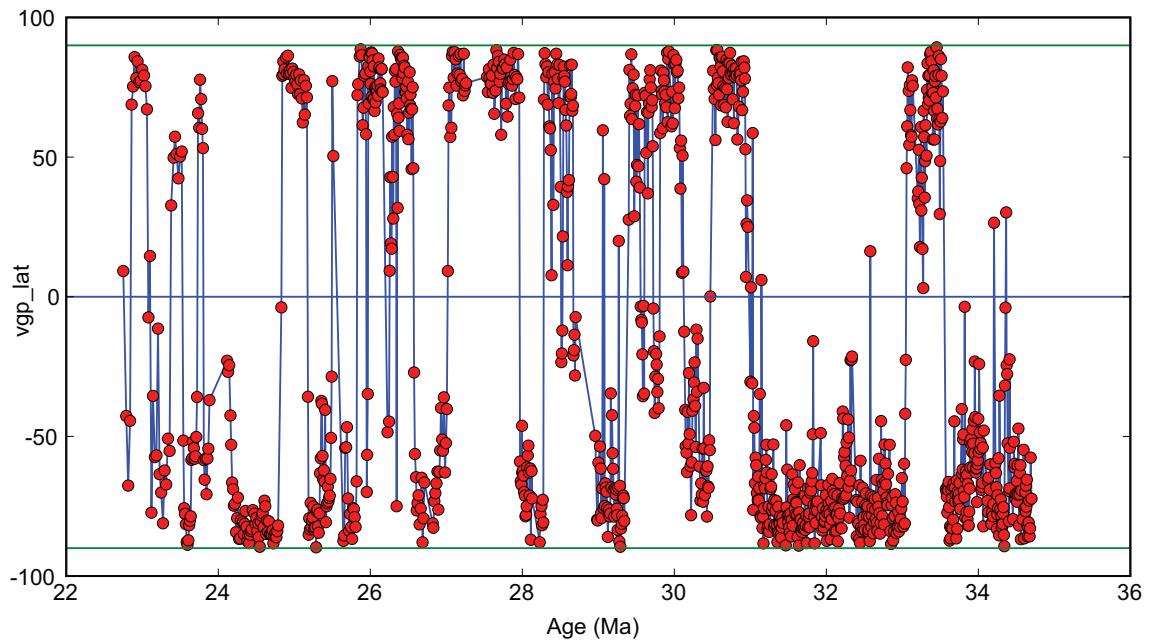
5.2.95 strip_magic.py

[Essentials Chapter 15] and [MagIC]

Follow the instructions for download_magic.py but search for Tauxe and Hartl and 1997. Download the smartbook (text file) and unpack it into a new directory using the **download_magic.py** command and the file *zmab0094214tmp02.txt* as the input file (in the Tauxe and Hartl directory). First run **strip_magic.py** to see what is available for plotting, then plot the inclination data versus depth (pos). Then plot the VGP latitudes versus age:

```
$ download_magic.py -f zmab0094214tmp03.txt
working on: 'er_locations'
er_locations data put in ./er_locations.txt
working on: 'er_sites'
er_sites data put in ./er_sites.txt
working on: 'er_samples'
.....
$ strip_magic.py
available objects for plotting: ['all']
available X plots: ['age', 'pos']
available Y plots: ['lon', 'int', 'lat']
available method codes: ['LP-PI-IRM', 'LP-PI-REL']
$ strip_magic.py -x pos -y int -mcd LP-PI-IRM
S[a]ve to save plot, [q]uit without saving: a
1 saved in strat.svg
%strip_magic.py -x age -y lat
S[a]ve to save plot, [q]uit without saving: a
1 saved in strat.svg
```

The last command made this plot:



5.2.96 sundec.py

[Essentials Chapter 9] [sundec docs]

Use the program **sundec.py** to calculate azimuth of the direction of drill. You are located at 35° N and 33° E. The local time is three hours ahead of Universal Time. The shadow angle for the drilling direction was 68° measured at 16:09 on May 23, 1994.

The program **sundec.py** works either by interactive data entry or by reading from a file.

Save the following in a file called *sundec_example.dat*:

```
3 35 33 1994 5 23 16 9 68
```

which is:

Δ_{GMT} lat lon year mon day hh mm shadow_angle

We can analyze this file with either:

```
$ sundec.py -f sundec_example.dat
154.2
```

or

```
$ sundec.py < sundec_example.dat
154.2
```

or by manual input:

```
$ sundec.py -i
Time difference between Greenwich Mean Time (hrs to ADD to
    GMT for local time):
<cntl-D> to quit 3
Year: <cntl-D to quit> 1994
Month: 5
Day: 23
hour: 16
minute: 9
Latitude of sampling site (negative in southern hemisphere): 35
Longitude of sampling site (negative for western hemisphere): 33
Shadow angle: 68
154.2
Time difference between Greenwich Mean Time (hrs to ADD to
    GMT for local time):
<cntl-D> to quit ^D
Good-bye
```

In any case, the declination is 154.2°.

5.2.97 thellier_magic.py

[Essentials Chapter 10] and [MagIC] [thellier_magic docs]

NB: This program is no longer maintained. You should try thellier_gui.py instead.

To see how **thellier_magic.py** works, download the text file from a recent paper by Shaar et al. (2011) from the MagIC database:

<http://earthref.org/MAGIC/doi/0.1016/j.epsl.2010.11.013>

Unpack the data with `download_magic.py`. The original interpretations are stored in a file called `pmag_specimens.txt`, but **thellier_magic.py** looks for a specimen file called `thellier_specimens.txt`. To create such a file, use the program `mk_redo.py` followed by `thellier_magic_redo.py`. Then you can take a look at the data using `thellier_magic.py` and change some of the interpretations, for example adding one for the specimen s2s0-01 which was rejected by Shaar et al. (2011). This has both non-linear TRM acquisition

and ATRM anisotropy data, so the corrections will have to be applied using `thellier_magic_redo.py` after exiting the `thellier_magic.py` program.

Here is a transcript of a session that does all this:

```
$ download_magic.py -f zmab0100159tmp01.txt
working on: 'er_locations'
er_locations data put in ./er_locations.txt
working on: 'er_sites'
er_sites data put in ./er_sites.txt
working on: 'er_samples'
er_samples data put in ./er_samples.txt
....
$ mk_redo.py
$ thellier_magic_redo.py
Processing 112 specimens - please wait
uncorrected thellier data saved in: ./thellier_specimens.txt

$ thellier_magic.py
.....
16      550    323.6    -4.9 4.370e-08      4.2
17      560    322.1    -2.5 3.240e-08      4.9
Looking up saved interpretation....
Saved interpretation:
specimen      Tmin  Tmax  N  lab_field  B_anc  b  q  f(coe)  Fvds  beta  MAD  Dang
s1p1-01      0  560 18 75.0 79.4 -1.059  54.2 0.919 0.897 0.015      2.0      1.5
pTRM direction=    210.8      85.0  MAD:      3.7
Saved interpretation:
specimen      Tmin  Tmax  N  lab_field  B_anc  b  q  f(coe)  Fvds  beta  MAD  Dang
s1p1-01      0  560 18 75.0 79.4 -1.059  54.2 0.919 0.897 0.015      2.0      1.5
pTRM direction=    210.8      85.0  MAD:      3.7
s[a]ve plot, set [b]ounds for calculation, [d]elete current interpretation
[p]revious, [s]ample, [q]uit:
Return for next specimen
s
```

```
Enter desired specimen name (or first part there of): s2s0-01
```

```
s2s0-01 214 of 269
```

index	step	Dec	Inc	Int	Gamma
0	0	194.5	-25.2	3.380e-07	
1	100	194.1	-25.2	3.360e-07	0.0
2	200	192.1	-25.4	3.330e-07	11.5
3	250	194.8	-25.5	3.290e-07	76.7
4	300	193.6	-25.3	3.070e-07	11.7
5	350	191.6	-26.7	1.460e-07	8.1
6	375	188.4	-33.6	3.420e-08	5.5
7	405	36.9	-27.6	6.800e-09	6.1
8	430	29.8	-12.9	2.930e-09	6.2

```
Looking up saved interpretation....
```

```
None found :(
```

```
s[a]ve plot, set [b]ounds for calculation, [d]elete current interpretation
```

```
Return for next specimen
```

```
b
```

```
Enter index of first point for calculation: [ 0 ]
```

```
return to keep default 0
```

```
Enter index of last point for calculation: [ 8 ]
```

```
return to keep default 8
```

```
Optimization terminated successfully.
```

```
    Current function value: 0.000000
```

```
    Iterations: 82
```

```
    Function evaluations: 157
```

```
Optimization terminated successfully.
```

```
    Current function value: 0.000000
```

```
    Iterations: 46
```

```
    Function evaluations: 89
```

```
Non-linear TRM corrected intensity= 79.7699845088
```

```
Save this interpretation? [y]/n
```

```
y
```

```
s2s0-02 215 of 269
```

index	step	Dec	Inc	Int	Gamma
0	0	295.5	-9.9	6.560e-07	
1	100	304.9	-10.1	6.480e-07	88.7
2	200	298.8	-10.5	6.420e-07	84.8

```

3      250    299.8   -10.5 6.330e-07    87.9
4      300    299.2   -10.5 5.860e-07    27.0
5      350    295.1    -9.5 2.270e-07    4.5
6      375    280.1   -21.7 4.940e-08    2.0
7      405    169.3   -16.3 1.450e-08    2.1
8      430    151.9   -15.5 1.070e-08    2.6

```

Looking up saved interpretation....

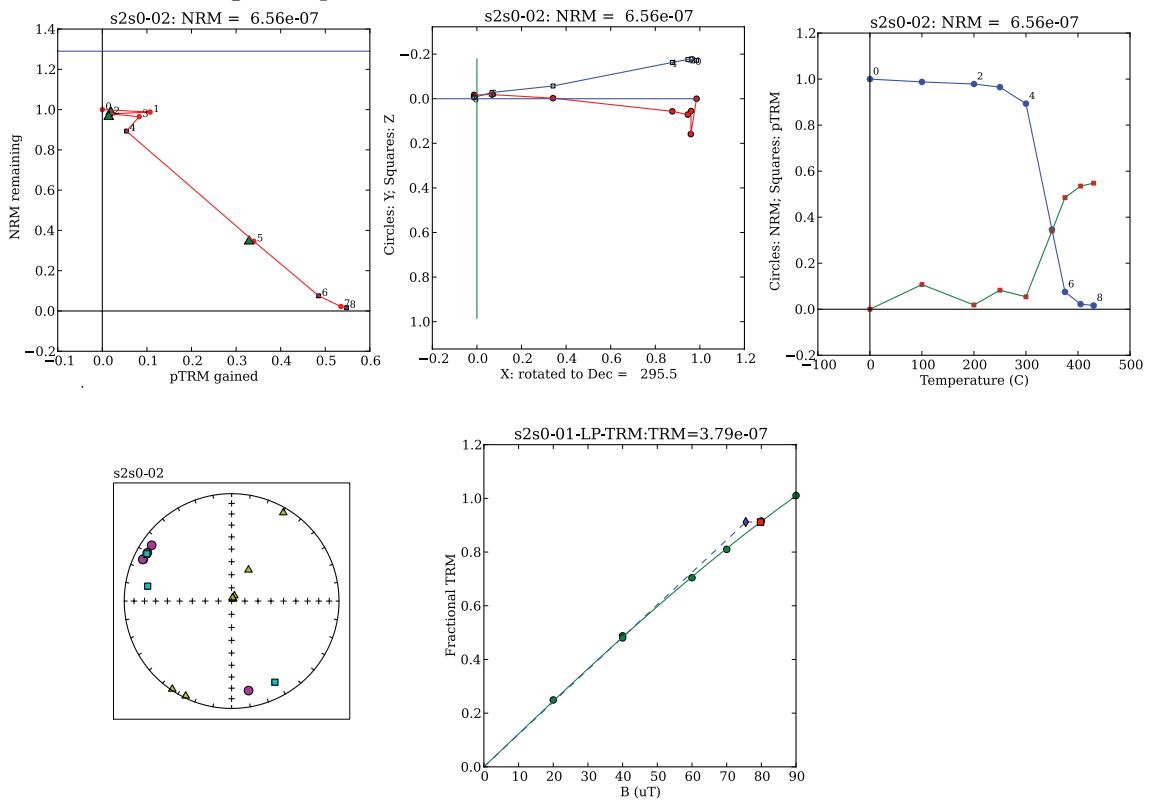
None found :(

s[a]ve plot, set [b]ounds for calculation, [d]elete current interpretation

Return for next specimen

q

You should have gotten plots that look like these:



When you exit the program, you will have modified the *thellier-specimens.txt* file to include the new interpretation.

5.2.98 thellier_magic_redo.py

[Essentials Chapter 10] and [MagIC] [thellier_magic_redo docs]

This program is no longer maintained. This function is embedded in thellier_gui.py when you import a specimen file.

This program allows the recalculation of paleointensity experimental data derived from Thellier type experiments. It allows correction for remanence anisotropy from AARM or ATRM ellipsoids (stored in *rmag_anisotropy* format files (see [Essentials Chapter 13] and the *aarm_magic.py* and *atrm_magic.py*) and non-linear TRM corrections, if TRM aquisition data are available (see also *trmaq_magic.py*).

Apply the corrections to the data you re-interpreted in the *thellier_magic.py* example, and create a new *pmag_specimens.txt* formatted file, use the program **thellier_magic_redo.py**. First, create a “redo” file using , then re-do the calculations using **thellier_magic_redo.py**, including anisotropy and non-linear TRM corrections. Combine all the specimen files into one using *combine_magic.py*.

```
$ mk_redo.py -f thellier_specimens.txt
$ thellier_magic_redo.py -ANI -NLT
Processing 112 specimens - please wait
WARNING: NO FTEST ON ANISOTROPY PERFORMED BECAUSE OF MISSING SIGMA - DOING CORRECTION ANYWAY
.....
anisotropy corrected data saved in: ./AC_specimens.txt
$ combine_magic.py -F pmag_specimens.txt -f thellier_specimens.txt AC_specimens.txt NLT_specimens.txt
File ./thellier_specimens.txt read in with 112 records
File ./AC_specimens.txt read in with 112 records
non-linear TRM corrected data saved in: ./NLT_specimens.txt
All records stored in ./pmag_specimens.txt
```

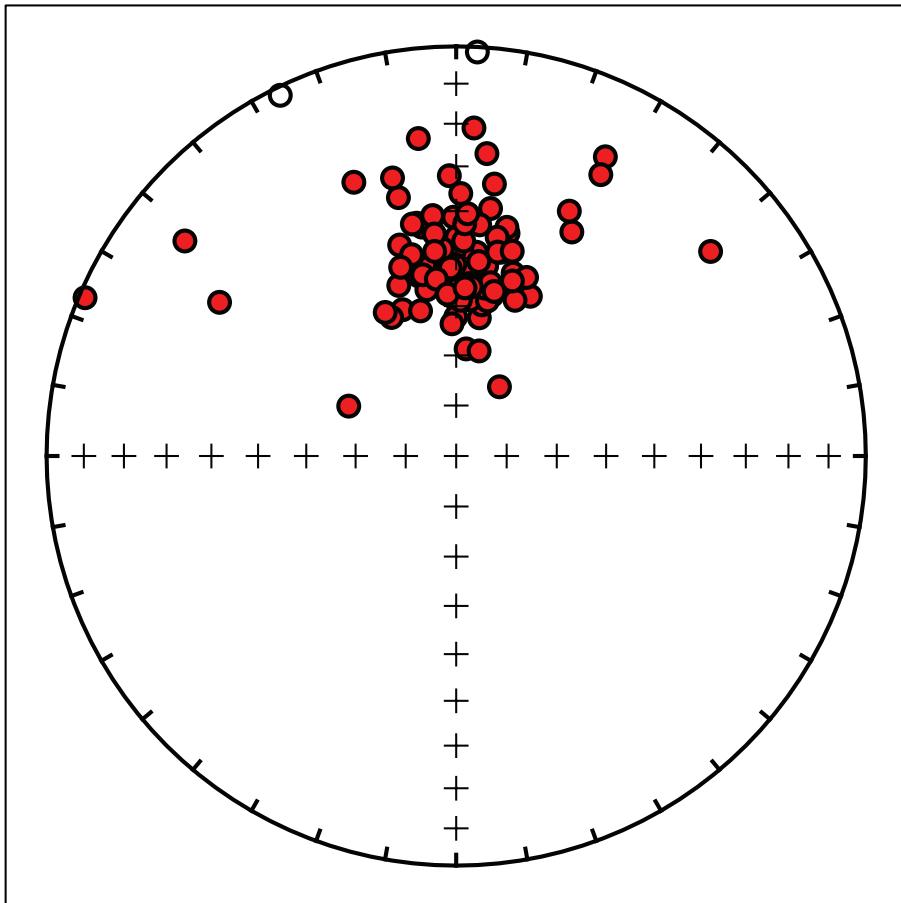
5.2.99 tk03.py

[Essentials Chapter 16] [tk03 docs]

Sometimes it is useful to generate a distribution of synthetic geomagnetic field vectors that you might expect to find from paleosecular variation of the geomagnetic field. The program **tk03.py** generates distributions of field vectors from the PSV model of Tauxe and Kent (2004). Use this program to generate a set of vectors for a latitude of 30° and plot them with *eqarea.py*.

```
$ tk03.py -lat 30 >tk03.out
$ eqarea.py -f tk03.out
```

which should give you a plot something like this:



5.2.100 uniform.py

[uniform docs]

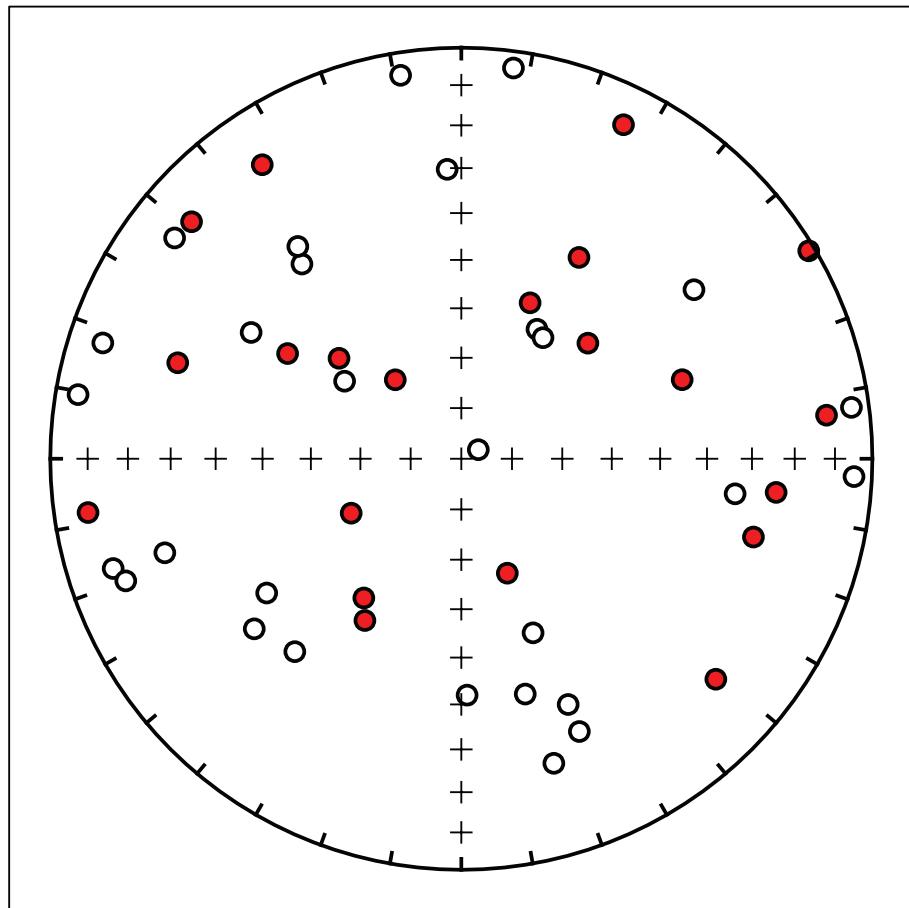
It is at times handy to be able to generate a uniformly distributed set of directions (or geographic locations). This is done using a technique described by Fisher et al. (1987).

Draw 50 directions from a uniform distribution and save to a file called *uniform.out*. Then plot the directions with *eqarea.py*:

```
$ uniform.py -F uniform.out -n 50  
$ eqarea.py -f uniform.out
```

which should yield a plot something (but not exactly) like this:

Equal Area Plot



5.2.101 update_measurements.py

[MagIC Database] [update_measurements docs]

This program is no longer maintained. This function is embedded in Pmag GUI.

In the SIO laboratory, our default specimen naming scheme has a logical relationship to the sample and site names. Sometimes there is no simple relationship and the MagIC import procedure can't parse the sample name into a site name, or the original concept of a site gets changed, for example if several lava flows turn out to be the same one. In any case, there must be a way to change the way data get averaged after the measurement data get converted to a `magic_measurements` formatted file. To do

this, the sample, site relationship can be established in the *er_sample.txt* file for example via the procedure described in *orientation_magic.py* documentation. After the correct relationships are in the *er_samples.txt* file, these must be propagated throughout the rest of the MagIC tables, starting with the *magic_measurements.txt* file. The program **update_measurements.py** will do this at the measurements level. *specimens_results_magic.py* will then propagate the changes through to the *pmag_results.txt* file.

5.2.102 upload_magic.py

[MagIC Database] [upload_magic docs]

This function is embedded in Pmag GUI.

This program takes all the MagIC formatted files and puts them into a file which can be imported into the MagIC console software for uploading into the MagIC database. As an example, we can “repackage” the file used file downloaded in the *download_magic.py* example. You could re-interpret that data or fix records with errors, then re-upload the corrected file.

In the *upload_magic* directory in the example *data_files* directory, someone has entered all the site latitudes as longitudes and vice versa (surprisingly common!). You can fix this in the *er_sites.txt* file, by swapping the headers *sample_lat*/*sample_lon* in the *er_samples.txt* file and *site_lat*/*site_lon* in the *er_sites.txt* file then run *specimens_results_magic.py* to propagate the changes through to the results table. Be sure to set the criteria switch (-exc), the latitude switch (-lat), the geographic coordinate switch (-crd g) and the age switch (-age 0 5 Ma). Then re-package the files for uploading.

AFTER fixing the *er_samples.txt* and *er_sites.txt* files, do the following:

```
$ specimens_results_magic.py -exc -lat -age 0 5 Ma -crd g
Acceptance criteria read in from pmag_criteria.txt
```

```
Pmag Criteria stored in pmag_criteria.txt
```

```
sites written to pmag_sites.txt
results written to pmag_results.txt
```

```
$ upload_magic.py
Removing: ['citation_label', 'compilation', 'calculation_type', 'average_n_lines',
'average_n_planes', 'specimen_grade', 'site_vgp_lat', 'site_vgp_lon', 'direction',
'specimen_Z', 'magic_instrument_codes', 'cooling_rate_corr', 'cooling_rate_mcd']
```

```
./er_expeditions.txt is bad or non-existent - skipping
file ./er_locations.txt successfully read in
er_locations written to ./upload.txt
file ./er_samples.txt successfully read in
only first orientation record from er_samples.txt read in
er_samples written to ./upload.txt
file ./er_specimens.txt successfully read in
only measurements that are used for interpretations
.....
now converting to dos file 'upload_dos.txt'
Finished preparing upload file
```

5.2.103 vdm_b.py

[Essentials Chapter 2] [vdm_b docs]

Use this program to try to recover the original field intensity b from a Virtual Dipole Moment of 71.59 ZAm² for the latitude 22°.

```
$ cat>vdm_b_example.dat
71.59e21 22
^D
$ vdm_b.py -f vdm_b_example.dat
3.300e-05
```

Compare this answer with the original in b_vdm.py, noting that the original input was in millitesla, while this is in tesla.

5.2.104 vector_mean.py

[Essentials Chapter 2] [vector_mean docs]

Create a set of vector data with tk03.py for a latitude of 30°N. Calculate the vector mean of these data.

```
$ tk03.py -lat 30 >vector_mean_example.dat
$ vector_mean.py -f vector_mean_example.dat
1.3    49.6    2.289e+06 100
```

5.2.105 vgp_di.py

[Essentials Chapter 2] [vgp_di docs]

Use the program **vgp_di.py** to convert the following:

λ_p	ϕ_p	λ_s	ϕ_s
68	191	33	243

Put the data into a file *vgp_di_example.dat* for example using **cat** on a *NIX operating system. Here is a transcript of one way to use the program which spits out declination, inclination:

```
$ vgp_di.py -f vgp_di_example.dat
335.6    62.9
```

Just for good measure, you could try it out on the data in the *di_vgp.py* example. See if you get the right answer!

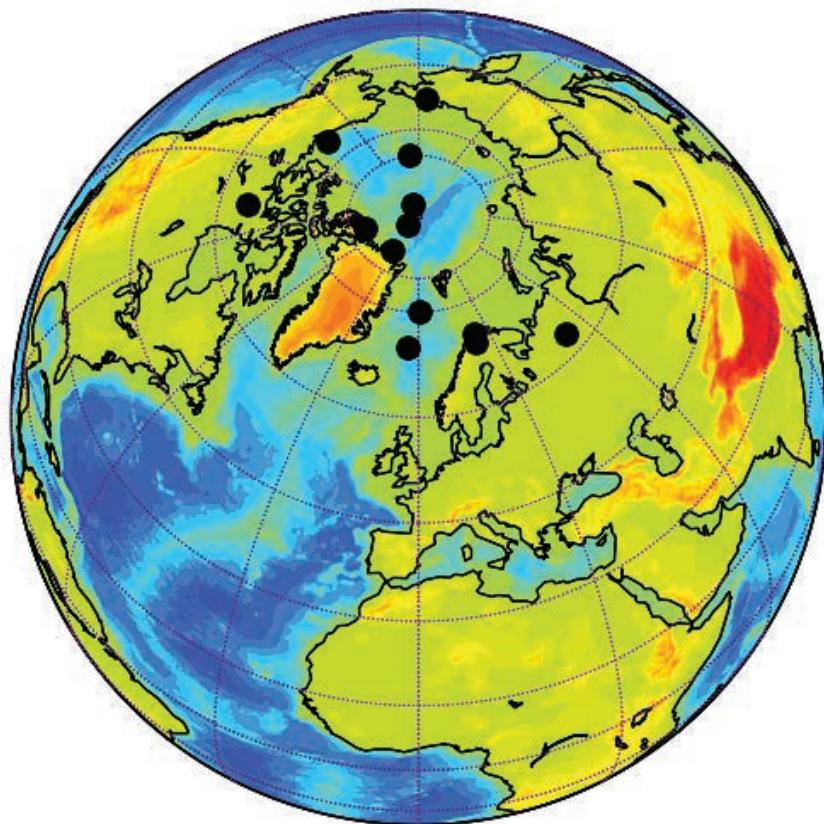
5.2.106 vgpmap_magic.py

[Essentials Chapter 2], [MagIC Database] and high resolution instructions [vgpmap_magic docs]

Make a plot of the VGPs calculated for the dataset downloaded in the *download_magic.py* example. Install the high resolution and the etopo20 data files. Use *install_etopo.py* for that. and plot the data on an orthographic projection with the viewpoint at 60°N and the Greenwich Meridian (longitude = 0). Make the points black dots with a size of 10pts. Save the file in png format

```
vgpmap_magic.py -crd g -prj ortho -eye 60 0 -etp -sym ko 10 -fmt png
S[a]ve to save plot, Return to quit: a
1 saved in VGP_map.png
```

You should have a plot like this one:



To use this program, you need to have basemap, which is not part of the free Python software distribution. Also, if you don't have the high resolution installed by `install_etopo.py`, just leave the `-etp` switch off to get a plain plot.

5.2.107 `watsonsF.py`

[Essentials Chapter 11] [watsonsF docs]

First generate two data files with `fishrot.py` with $\kappa = 15$, $N = 10$ and $I = 42$, with $D = 10$. for the first and 20 for the second:

```
$ fishrot.py -k 15 -n 10 -I 42 -D 10 >watsonsF_example_file1.dat
$ fishrot.py -k 15 -n 10 -I 42 -D 20 > watsonsF_example_file2.dat
```

To compare these two files using **watsonsF.py**:

```
$ watsonsF.py -f watsonsF_example_file1.dat -f2 watsonsF_example_file2.dat
7.74186876032 3.2594 3.2594
```

The first number is Watson's F statistic for these two files (see Essentials Chapter 11) and the second is the number to beat for the two files to be drawn from the same fisher distribution (share a common mean). In this case the data fail this test (F is greater than the required number). Your results may vary!

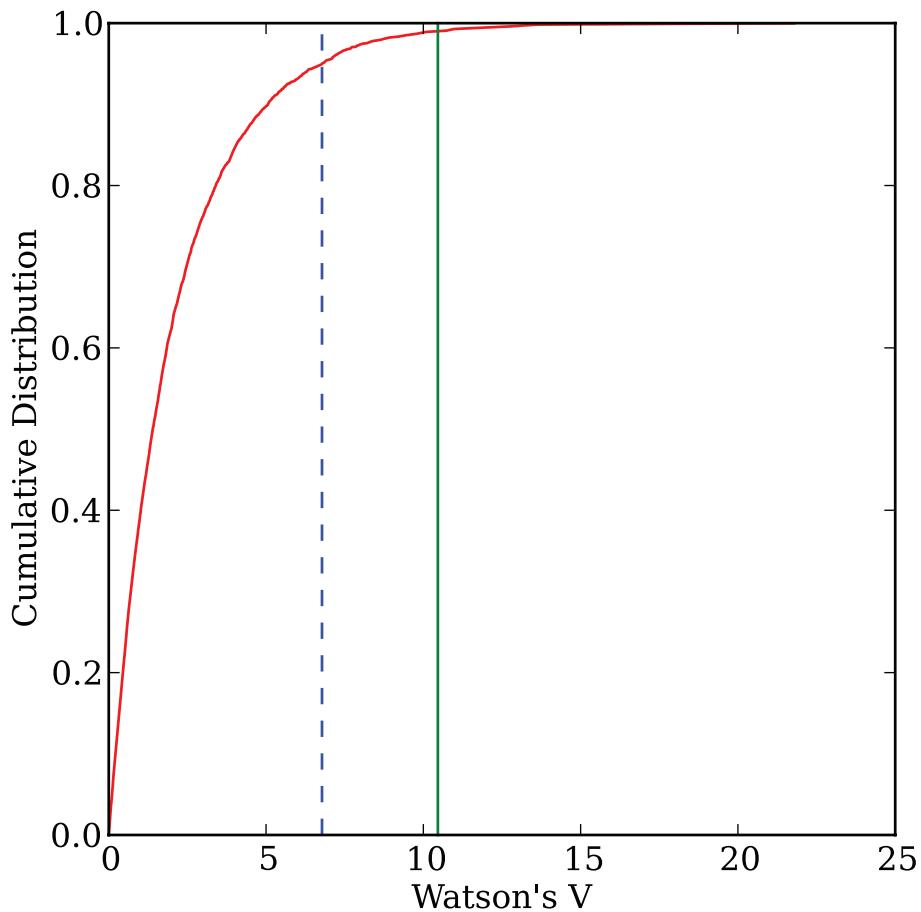
5.2.108 watsonsV.py

[Essentials Chapter 11] [watsonsV docs]

Use the two data files generated in the example for **watsonsF.py** and repeat the test using Watson's V_w statistic.

```
$ watsonsV.py -f watsonsF_example_file1.dat -f2 watsonsF_example_file2.dat
Doing 5000 simulations
50
100
150
200
...
Watson's V, Vcrit:
      10.5      6.8
S[a]ve to save plot, [q]uit without saving: a
1 saved in WatsonsV_watsonsF_example_file1.dat_watsonsF_example_file2.dat.svg
```

which generates the plot:



The two files are significantly different because Watson's V (10.5 in this example) is greater than the V_{crit} value estimated using Monte Carlo simulation (6.8).

Note that your results may vary in detail because every instance of **fishrot.py** generates a different randomly drawn dataset.

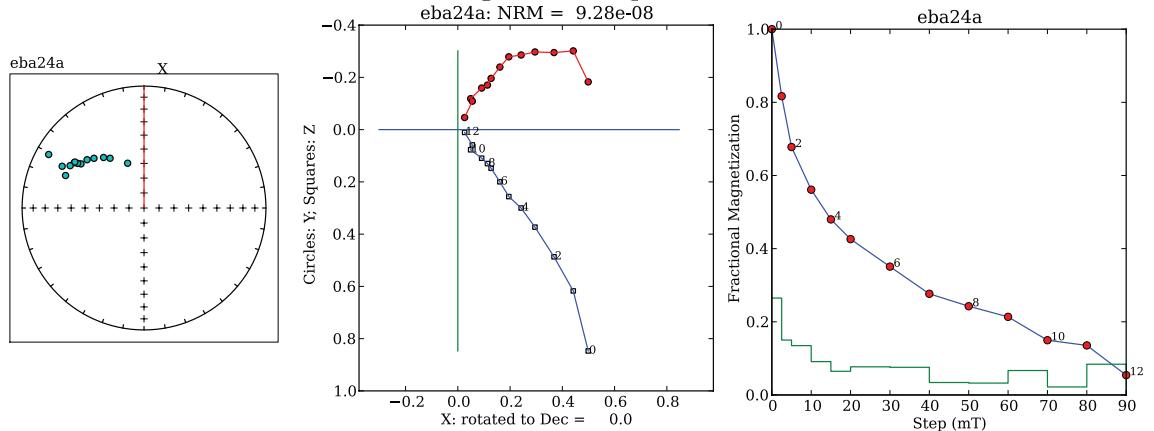
5.2.109 zeq.py

[Essentials Chapter 9] [zeq docs]

Use the program **zeq.py** to 1) plot a Zijderveld diagram of the data in *zeq-example.txt*. b) Calculate a best-fit line from 15 to 90 mT. c) Rotate the data such that the best-fit line is projected onto the horizontal axis (instead of the default, North). d) Calculate a best-fit plane from 5 to 80 mT. Save these plots.

```
$ zeq.py -f zeq_example.dat -u mT
```

By selecting 'b', you can pick the bounds and choose 'l' for best-fit line or 'p' for best-fit plane. You can rotate the X-Y axes by selecting 'h' and setting the X axis to 312. Finally, you can save your plots with the 'a' option. You should have saved something like these plots:



The equal area projection has the X direction (usually North in geographic coordinates) to the top. The red line is the X axis of the Zijderveld diagram. Solid symbols are lower hemisphere. The solid (open) symbols in the Zijderveld diagram are X,Y (X,Z) pairs. The demagnetization diagram plots the fractional remanence remaining after each step. The green line is the fraction of the total remanence removed between each step.

5.2.110 zeq_magic.py

[Essentials Chapter 9] & [MagIC Database] [zeq_magic docs]

This program is no longer maintained and has been superseded by Demag GUI.

Plot the AF demagnetization data available in the file you got in the `download_magic.py` example using `zeq_magic.py`. Use geographic coordinates, where orientations are available.

```
$ zeq_magic.py -crd g
sr01a1 0 out of 177
      looking up previous interpretations...
Specimen   N      MAD      DANG    start     end      dec      inc  type component
sr01a1 9      1.8      1.2  2000.0  550.0  331.0  64.4  DE-BFL  A
g: 0      0.0  C  4.065e-05  324.1      66.0
```

```

g: 1    100.0  C  3.943e-05   330.5   64.6
g: 2    150.0  C  3.908e-05   324.9   65.5
g: 3    200.0  C  3.867e-05   329.4   64.6
g: 4    250.0  C  3.797e-05   330.3   64.5
g: 5    300.0  C  3.627e-05   330.1   64.0
g: 6    350.0  C  3.398e-05   327.0   64.4
g: 7    400.0  C  2.876e-05   328.2   64.0
g: 8    450.0  C  2.148e-05   323.8   65.2
g: 9    500.0  C  1.704e-05   326.0   63.9
g: 10   525.0  C  1.200e-05   326.5   63.7
g: 11   550.0  C  5.619e-06   325.5   64.4

```

g/b: indicates good/bad measurement. ‘‘bad’’ measurements excluded from calculation

```

set s[a]ve plot, [b]ounds for pca and calculate, [p]revious, [s]pecimen,
      change [h]orizontal projection angle,   change [c]oordinate systems,
[d]elete current interpretation(s), [e]dit data,   [q]uit:

```

<Return> for next specimen

The plots will look similar to the `zeq.py` example, but the default here is for the X-axis to be rotated to the specimen’s NRM direction (note how the X direction is rotated off from the top of the equal area projection).

5.2.111 `zeq_magic_redo.py`

[Essentials Chapter 9] & [MagIC Database] [`zeq_magic_redo` docs]

The functionality of this program has been incorporated into Demag GUI so you should use that.

In the `zeq-magic` directory, use the program `zeq_magic_redo.py` to create a `pmag-specimens` formatted file with data in geographic coordinates from the sample coordinate file `zeq-specimens.txt`. Assuming that sample orientations are in a file called `er_samples.txt`, use `mk_redo.py` first to create file called `zeq_redo`. Then use `zeq_magic_redo.py` to create two `pmag-specimen` formatted files: one in specimen coordinates `zeq-specimens-s.txt` and one in geographic coordinates `zeq-specimens-g.txt`. Combine these into one file called `pmag-specimens.txt`.

Note that indented lines belong with the line above as a single line.

```
$ mk_redo.py  
$ zeq_magic_redo.py -F zeq_specimens_s.txt -crd s  
Processing 175 specimens - please wait  
Recalculated specimen data stored in ./zeq_specimens_s.txt  
  
$ zeq_magic_redo.py -F zeq_specimens_g.txt -crd g  
Processing 175 specimens - please wait  
Recalculated specimen data stored in ./zeq_specimens_g.txt  
$ combine_magic.py -F pmag_specimens.txt -f zeq_specimens_s.txt zeq_specimens_g.txt
```

5.3 Complaints department

The best way to raise issues with any of the software or its documentation is to post to the issues page of the Github project: <https://github.com/ltauxe/PmagPy/issues>. Lisa Tauxe (ltauxe@usd.edu) can also be contacted by email with bug reports, suggestions and requests.

Chapter 6

The MagIC database and file formats

A number of the programs in **PmagPy** were developed to take advantage of the MagIC database and aid getting data in and out of it. So, we need some basic understanding of what MagIC is and how it is structured. MagIC is an Oracle database that is part of the EarthRef.org collection of databases and digital reference material. Anyone interested in the MagIC database should first become a registered EarthRef.org user. To do this, go to <http://earthref.org> and click on the **Register** link in the **Topmenu**. Registration is not required for access to data or browsing around, but is required for uploading of data into the MagIC database, something which we sincerely hope you will have a chance to do. After you register, go to <http://earthref.org/MAGIC/search>.

You can download data using the MagIC search website. After downloading, the data can be unpacked and examined using various tools in the **PmagPy** package, for example using Pmag GUI.

Paleomagnetic and rock magnetic data are collected and analyzed in a wide variety of ways with different objectives. Data sets can be extremely large or can be the barest boned data summaries published in legacy data tables. The goal of MagIC has been to have the flexibility to allow a whole range of data including legacy data from publications or other databases to new studies which include all the measurements, field photos, methodology, and so on. The general procedure for the future will be to archive the data at the same time that they are published. So, to smooth the path, it is advisable to put your data into the MagIC format as early in the process as possible. All data that enters the database must be converted to the

standard MagIC format either as a set of MagIC tables, or as one combined text file. These can then be uploaded into the MagIC database.

6.1 Structure of the database tables

The MagIC database is organized around a series of data tables. The complete data model can be found here: <http://earthref.org/MAGIC/metadata.htm>.

Each MagIC table has a one line header of the form:

tab **table_name**

“tab” (or “tab delimited”) means that the table is tab delimited. In theory other delimiters are possible, but **PmagPy** only uses tab delimited formats. The **table_name** is one of the table names. The tables are of four general types: EarthRef tables (**er_**) shared in common with other EarthRef databases, MagIC tables (**magic_**) common to both rock magnetic and paleomagnetic studies, Paleomagnetic tables (**pmag_**), data reduction useful in paleomagnetic studies, Rock magnetic tables (**rmag_**), data reduction useful for rock magnetic studies. Most studies use only some of these tables. Here are some useful tables for a typical paleomagnetic study (starred are required in all cases):

table	Brief description
er_locations*	geographic information about the location(s) of the study
er_sites	locations, lithologic information, etc. for the sampling sites
er_samples	orientation, sampling methods, etc. for samples
er_specimens	specimen weights, volumes
er_ages	age information.
er_images	images associated with the study (field shots, sample photos, photomicrographs, SEM images, etc.)
er_mailinglist	contact information for people involved in the study
magic_measurements	measurement data used in the study
magic_instruments	instruments used in the study
pmag_specimens	interpretations of best-fit lines, planes, paleointensity, etc.
pmag_samples	sample averages of specimen data
pmag_sites	site averages of sample data
pmag_results	averages, VGP/V[A]DM calculations, stability tests, etc.
pmag_criteria	criteria used in study for data selection
rmag_susceptibility	experiment for susceptibility parameters
rmag_anisotropy	summary of anisotropy parameters
rmag_hysteresis	summary of hysteresis parameters
rmag_remanence	summary of remanence parameters
rmag_results	summary results and highly derived data products (critical temperatures, etc.)
rmag_criteria	criteria used in study for data selection

The second line of every file contains the column headers (meta-data) describing the included data. For example, an **er_sites** table might look like this:

tab	er_sites					
	er_site_name	er_location_name	site_lithology	site_type	site_lat	site_lon
AZ01	Azores	basalt	lava flow	37.80	-25.80	
...						

Although data can be entered directly into Excel spreadsheets by hand, it is easier to generate the necessary tables as a by-product of ordinary data processing without having to know details of the meta-data and method codes. The section on PmagPy describes how to use the **PmagPy** software for data analysis and generate the MagIC data tables automatically for the most common paleomagnetic studies involving directions and/or paleointensities. See also Pmag GUI.

6.2 A word about method codes

The MagIC database tags records with “method codes” which are short codes that describe various methods associated with a particular data record. The complete list is available here: <http://earthref.org/MAGIC/methods.htm>. Most of the time, you do not need to know what these are (there are over a hundred!), but it is helpful to know something about them. These are divided into several general categories like ‘geochronology methods’ and ‘field sampling methods’. Method codes start with a few letters which designate the category (e.g., GM or FS for geochronology and field sampling respectively). Then there is a second part and possibly also a third part to describe methods with lesser or greater detail. The current (version 2.4) method codes that describe various lab treatment methods to give you a flavor for how they work are listed in this table:

LT-AF-D	Lab Treatment	Alternating field: Double demagnetization with AF along X,Y,Z measurement followed by AF along -X,-Y,-Z measurement
LT-AF-G	Lab Treatment	Alternating field: Triple demagnetization with AF along Y,Z,X measurement followed by AF along Y and AF along Z measurement
LT-AF-I	Lab Treatment	Alternating field: In laboratory field
LT-AF-Z	Lab Treatment	Alternating field: In zero field
LT-CHEM	Lab Treatment	Cleaning of porous rocks by chemical leaching with HCl
LT-FC	Lab Treatment	Specimen cooled with laboratory field on
LT-HT-I	Lab Treatment	High temperature treatment: In laboratory field
LT-HT-Z	Lab Treatment	High temperature treatment: In zero field
LT-IRM	Lab Treatment	IRM imparted to specimen prior to measurement
LT-LT-I	Lab Treatment	Low temperature treatment: In laboratory field
LT-LT-Z	Lab Treatment	Low temperature treatment: In zero field
LT-M-I	Lab Treatment	Using microwave radiation: In laboratory field
LT-M-Z	Lab Treatment	Using microwave radiation: In zero field
LT-NO	Lab Treatment	No treatments applied before measurement
LT-NRM-APAR	Lab Treatment	Specimen heating and cooling: Laboratory field anti-parallel to the NRM vector
LT-NRM-PAR	Lab Treatment	Specimen heating and cooling: Laboratory field parallel to the NRM vector
LT-NRM-PERP	Lab Treatment	Specimen heating and cooling: Laboratory field perpendicular to the NRM vector
LT-PTRM-I	Lab Treatment	pTRM tail check: After zero field step, perform an in field cooling
LT-PTRM-MD	Lab Treatment	pTRM tail check: After in laboratory field step, perform a zero field cooling at same temperature
LT-PTRM-Z	Lab Treatment	pTRM tail check: After in laboratory field step, perform a zero field cooling at a lower temperature
LT-T-I	Lab Treatment	Specimen cooling: In laboratory field
LT-T-Z	Lab Treatment	Specimen cooling: In zero field
LT-VD	Lab Treatment	Viscous demagnetization by applying MU-metal screening
LP-X	Lab Treatment	Susceptibility
LT-ZF-C	Lab Treatment	Zero field cooled, low temperature IRM imparted
LT-ZF-CI	Lab Treatment	Zero field cooled, induced M measured on warming

For uploading to the database, all the individual tables should be assembled into a single file. Each individual data table is separated from the next by a series of '>>>>>>>' symbols, so a typical upload file might look like this:

```
tab er_locations
location_type er_citation_names location_end_lat location_begin_lon
er_location_name location_begin_lat location_end_lon
Drill Site This study 19.0 156.0 801C 19.0 156.0
Drill Site This study 19 156 801 19 156
>>>>>>
tab er_samples
er_citation_names sample_lithology er_site_name er_sample_name sample_type
er_location_name sample_lat sample_lon sample_class
This study Submarine Basaltic Glass 16r5113 16r5113 Lava Flow 801C
19 156 Igneous: Extrusive
This study Submarine Basaltic Glass 17r1026 17r1026 Lava Flow 801C
19 156 Igneous: Extrusive
.
.
.
```

Correctly formatted MagIC data tables can be assembled into a suitable upload text file by using the program `upload_magic.py` which reads in all MagIC tables in a given directory and puts them together as in the above example. You can invoke `upload_magic.py` on the command line or call it within Pmag GUI. `upload_magic.py` creates a file called `upload_magic.txt` which can be uploaded into the MagIC database.

Chapter 7

Introduction to Python Programming

Type 'python' on your command line.

You have just fired up Python and you are in an interactive mode with the prompt `>>>`. Now, you can just start typing commands. After each command, press the return key and see what happens:

```
>>> a=2
>>> a
2
>>> b=2
>>> c=a+b
>>> c
>>> c+=1
>>> c
5
>>> a=2; b=2; c=a+b; c
4
>>> d,e,f=4,5,6 # note syntax! d=4;e=5;f=6
>>> # note also that the symbol '#' means the rest of the line is a comment!
```

To get out of Python interactive mode and back to your beloved command line, type the control key (here-after `^`) and `D` at the same time. From your school experience of Algebra, you will recognize a, b , and c in the above session as *variables* and $+$ as an *operation*. If you have previous programming experience, you may have been surprised that we didn't

declare variables up front (C programmers always have to). And, the variables above are obviously behaving as integers, not floating point variables (no decimals) but they are not letters between i and n . And there were funny lines that seemed to set three numbers at once:

```
>>> a=2; b=2; c
and
>>> d,e,f=4,5,6 # note syntax! d=4;e=5;f=6
```

Here are some rules governing variables and operations in Python:

- Variable names are composed of alphanumeric characters, including ‘-’ and ‘_’.
- They are case sensitive: ‘a’ is not the same as ‘A’.
- They do NOT have to be specified in advance (unlike C)
- In fortran, integers are $i - n$ and floating points are all else - not the case in Python. You can make them whatever you want.
- + adds, - subtracts, * multiplies, / divides, % gives the remainder, ** raises to the power
- These two are fun: `+=` and `-=`. They add to and subtract from respectively.
- Parentheses determine order of operation (as in any reasonable programming language).
- For math functions, we can use various modules that either come standard with python (the math module) or are additions that come with the Enthought Python Edition we are using (the NumPy module). A module is just a collection of functions. NB: There is online help for any python function or method: just type `help(FUNC)`.

7.1 A first look at NumPy

O.K. First of all - how do you pronounce ‘NumPy’. According to Important People at Enthought (e.g, Robert Kern), it should be pronounced “Num” as in “Number” and “Pie” as in, well, pie, or Python. Oops. It is way more fun to say Numpee!

So, that out of the way, what can NumPy do for us? Turns out, a whole heck of a lot! But for now we will just scratch the surface. It can, for example, give us the value of π as `numpy.pi`. Note how the module name comes first, then the name of the function we wish to use. In this case, the function just returns the value of π .

To use NumPy functions, we must first “import” the module with the command `import`. The first time you do this after installing Python, it may take a while, but after that it should be very quick.

There are four styles of the import command which all do pretty much the same thing but differ in how you have to call the function after importing:

```
>>> import numpy  
>>> numpy.pi  
3.1415926535897931
```

This makes all the functions in NumPy available to you, but you have to call them with the `numpy.FUNC` syntax.

```
>>> import numpy as np # or anything else! e.g., some use: N  
>>> np.pi # or N.pi in the second case.  
3.1415926535897931
```

This does the same as the first, but allows you to call NumPy anything you want - to save typing? To import all the functions from NumPy and not have to type `numpy` at all:

```
>>> from numpy import *  
>>> pi  
3.1415926535897931
```

This imports all the umpty-ump functions, which is a heavy load on your memory, but you can also just import a few, like `pi` or `sqrt`:

```
>>> from numpy import pi, sqrt # pi and square root  
>>> pi  
3.1415926535897931  
>>> sqrt(4)  
2.0
```

Did you notice how `sqrt(4)` where 4 was an integer, returned a floating point variable (2.0)?

Good housekeeping Tip #1: We tend to import modules using the first option above. That way we know what module the functions I'm using are coming from - especially because we don't know off-hand ALL the functions available in any given module and there might be conflicts with my own function names or two different modules could have the same function (like `math` and `numpy`).

Here is a (partial) list of some useful `NumPy` functions:

<code>absolute(x)</code>	absolute value
<code>arccos(x)</code>	arccosine
<code>arcsin(x)</code>	arcsine
<code>arctan(x)</code>	arctangent
<code>arctan2(y,x)</code>	arctangent of y/x in correct quadrant (**very useful!)
<code>cos(x)</code>	cosine
<code>cosh(x)</code>	hyperbolic cosine
<code>exp(x)</code>	exponential
<code>log(x)</code>	natural logarithm
<code>log10(x)</code>	base 10 log
<code>sin(x)</code>	sine
<code>sinh(x)</code>	hyperbolic sine
<code>sqrt(x)</code>	square root
<code>tan(x)</code>	tangent
<code>tanh(x)</code>	hyperbolic tangent

Note that in the trigonometric functions, the argument is in RADIANS!. You can convert from degrees to radians by multiplying by: `numpy.pi/180..` Also notice how these functions have parentheses, as opposed to `numpy.pi` which has none. The difference is that these take arguments, while `numpy.pi` just returns the value of π .

If you are desperate, you can always use your Python interpreter as a calculator:

```
>>> import numpy
>>> a=2
>>> b=-12
>>> c=16
>>> quad1 = (-b + numpy.sqrt(b**2-4.*a*c))/(2.*a)
>>> quad1
4
>>> y=numpy.sin(numpy.pi/6.)
>>> y
0.5
```

7.2 Variable types

The time has come to talk about variable types. We've been very relaxed up to now, because we don't have to declare them up front and we can often even change them from one type to another on the fly. But - variable types matter, so here goes. Python has integer, floating point (both long and short), string and complex variable types. It is pretty clever about figuring out what is required. Here are some examples:

```
>>> number=1 # an integer
>>> Number=1.0 # a floating point
>>> NUMBER='1' # a string
>>> complex=1j # a complex number with imaginary part 1
>>> complex(3,1) # the complex number 3+1i
```

Try doing math with these!

```
>>> number+number
2      [ an integer]
>>> number+Number
2.0    [ a float]
>>> NUMBER+NUMBER
11 [a string]
>>> number+NUMBER  [Gives you an angry error message]
```

Lesson learned: you can't add a number and a string. and string addition is different! But you really have to be careful with this. If you multiply a float by an integer, it is possible that you will convert the float to an integer when you really wanted all those numbers after the decimal! So, if you want a float, use a float.

You can convert from one type to another (if appropriate) with:

```
int(Number); str(number); float(NUMBER);
long(Number); complex(real,imag)
```

`long()` converts to a double precision floating point and `complex()` converts the two parts to a complex number.

There is another kind of variable called "boolean". These are: `true`, `false`, `and`, `or`, and `not`. For the record, the integer '1' is `true` and '0' is `false`. These can be used to control the flow of the program as we shall learn later.

7.3 Data Structures

In previous programming experience, you may have encountered arrays, which are a nice way to group a sequence of numbers that belong together. In Python we also have arrays, but we also have more flexible data structures, like lists, tuples, and dictionaries, that group arbitrary variables together, like strings and integers and floats - whatever you want really. We'll go through some attributes of the various data structures, starting with lists.

Lists

- Lists are denoted with square brackets, [], and can contain any arbitrary set of items, including other lists!
- Items in the list are referred to by an index number, starting with 0.
- You can count from the end to the beginning by starting with -1 (the last item in the list), -2 (second to last), etc.
- Items can be sorted, deleted, inserted, sliced, counted, concatenated, replaced, added on, etc.

Examples:

```
>>> mylist=['a',2.0,'400','spam',42,[24,2]] # defines a list
>>> mylist[2] # refers to the third item
'400'
>>> mylist[-1] # refers to the last item
[24,2]
>>> mylist[1]=26.3 # replaces the second item
>>> del mylist[3] # deletes the fourth element
```

To slice out a chunk of the middle of a list:

```
>>> newlist=mylist[1:3]
```

This takes items 2 and 3 out (note it takes out up to but not including the last item number - don't ask me why). Or, we can slice it this way:

```
>>> newlist=mylist[3:]
```

which takes from the fourth item (starting from 0!) to the end.

To copy a list BEWARE! You can make a copy - but it isn't an independent copy (like in, e.g., Fortran), but it is just another name for the SAME OBJECT, so:

```
>>> mycopy=mylist  
>>>mylist[2]='new'  
>>>mycopy[2]  
'new'
```

See how `mycopy` got changed when we changed `mylist`? To spawn a new list that is a copy, but an independent entity:

```
>>>mycopy=mylist[:]
```

Now try:

```
>>>mylist[2]=1003  
>>>mycopy[2]  
'new'
```

So now `mycopy` stayed the way it was, even as `mylist` changed.

Python is “object oriented”, a popular concept in coding circles. We’ll learn more about what that means later, but for right now you can walk around feeling smug that you are learning an object oriented programming language. O.K., what is an object? Well, `mylist` is an object. Cool. What do objects have that might be handy? Objects have “methods” which allow you to do things to them. Methods have the form: `object.method()`. Here are two examples:

```
>>> mylist.append('me too') # appends a string to mylist  
>>> mylist.sort() # sorts the list alphanumerically  
>>> mylist  
[2.0, 42, [24, 2], '400', 'a', 'me too', 'spam']
```

For a complete list of methods for lists, see: <http://docs.python.org/tutorial/datastructures.html>

More about strings

Numbers are numbers. While there are more kinds of numbers (complex, etc.), strings can be more interesting. Unlike in some languages, they can be denoted with single, double or triple quotes: e.g., ‘spam’, “Sam’s spam”, or

```
.....  
Hi there we can type as  
many lines as we want  
.....
```

Strings can be added together (`newstring = 'spam' + 'alot'`). They can be sliced (`newerstring = newstring[0:3]`). but they CANNOT be changed in place - you can't do this: `newstring[0]='b'`. To find more of the things you can and cannot do to strings, see:

<http://docs.python.org/tutorial/introduction.html#strings>

Data structures as objects

Tuples

What? Tuples? Tuples consist of a number of values separated by commas. They are denoted with parentheses.

```
>>> t = 1234, 2.0, 'hello'
>>> t
(1234, 2.0, 'hello')
>>> t[0]
1234
```

Tuples are sort of like lists, but like strings, their elements cannot be changed. However, you can slice, concatenate, etc. For more see:

<http://docs.python.org/tutorial/datastructures.html#tuples-and-sequences>

Dictionaries!

Dictionaries are denoted by `{}`. They are also somewhat like lists, but instead of integer indices, they use alphanumeric 'keys': I love dictionaries. So here is a bit more about them.

To define one:

```
>>> Telnos={'lisa':46084,'lab':46531,'jeff':44707} # defines a dictionary
```

To return the value associated with a specific key:

```
>>> Telnos['lisa']
46084
```

To change a key value:

```
>>> Telnos['lisa']=46048
```

To add a new key value:

```
>>> Telnos['newguy']=48888
```

Dictionaries also have some methods. One useful one is:

```
>>> Telnos.keys()  
['lisa', 'lab', 'jeff', 'newguy']
```

which returns a list of all the keys.

For a more complete accounting of dictionaries, see:

<http://docs.python.org/tutorial/datastructures.html#dictionaries>

N-dimensional arrays

Arrays in Python have many similarities to lists. Unlike lists, however, arrays have to be all of the same data type (dtype), usually numbers (integers or floats), although there appears to be something called a character array. Also, the size and shape of an array must be known *a priori* and not determined on the fly like lists. For example we can define a list with `L=[]`, then append to it as desired, but not so arrays - they are much pickier and we'll see how to set them up later.

Why use arrays when you can use lists? They are far more efficient than lists particularly for things like matrix math. But just to make things a little confusing, there are several different data objects that are loosely called arrays, e.g., arrays, character arrays and matrices. These are all subclasses of ndarray. I'm just going to briefly introduce arrays and matrices here.

Here are a few ways of making arrays:

```
>>> import numpy  
>>> A= numpy.array([[1,2,3],[4,2,0],[1,1,2]])  
>>> A  
array([[1, 2, 3],  
       [4, 2, 0],  
       [1, 1, 2]])  
>>> B=numpy.arange(0,10,1).reshape(2,5)  
>>> B  
array([[0, 1, 2, 3, 4],  
       [5, 6, 7, 8, 9]])  
>>> C=numpy.array([[1,2,3],[4,5,6]],numpy.int32)  
>>> C  
array([[1, 2, 3],  
       [4, 5, 6]])  
>>> D=numpy.zeros((2,3)) # Notice the zeros and the size is specified by a tuple.  
>>> D
```

```

array([[ 0.,  0.,  0.],
       [ 0.,  0.,  0.]])
>>> E=numpy.ones((2,4))
>>> E
array([[ 1.,  1.,  1.,  1.],
       [ 1.,  1.,  1.,  1.]])
>>> F=numpy.linspace(0,10,14)
>>> F
array([ 0.          ,  0.76923077,  1.53846154,  2.30769231,
        3.07692308,  3.84615385,  4.61538462,  5.38461538,
        6.15384615,  6.92307692,  7.69230769,  8.46153846,
        9.23076923,  10.         ])
>>> G=numpy.ndarray(shape=(2,2), dtype=float)
>>> G # note how this is initialized with really low numbers (but not zeros).
array([[ 1.90979621e-313,  2.75303490e-308],
       [ 1.08539798e-071,  3.05363949e-309]])

```

Note the difference between `linspace(start,stop,N)` and `arange(start,stop,step)`. The function `linspace` creates an array with 14 evenly spaced elements between the start and stop values while `arange` creates an array with elements at colorbluestep intervals between the starting and stopping values. In some of the online examples you will find the short-cuts for `arange()` and `linspace` as `r_(-5,5,20j)` and `r_(-5,5,1.)` respectively.

Python arrays have methods like `dtype`, `ndim`, `shape`, `size`, `reshape()`, `ravel()`, `transpose()` etc. Did you notice how some of these require parentheses and some don't? The answer is that some of these are functions and some are classes, both of which we will get to later.

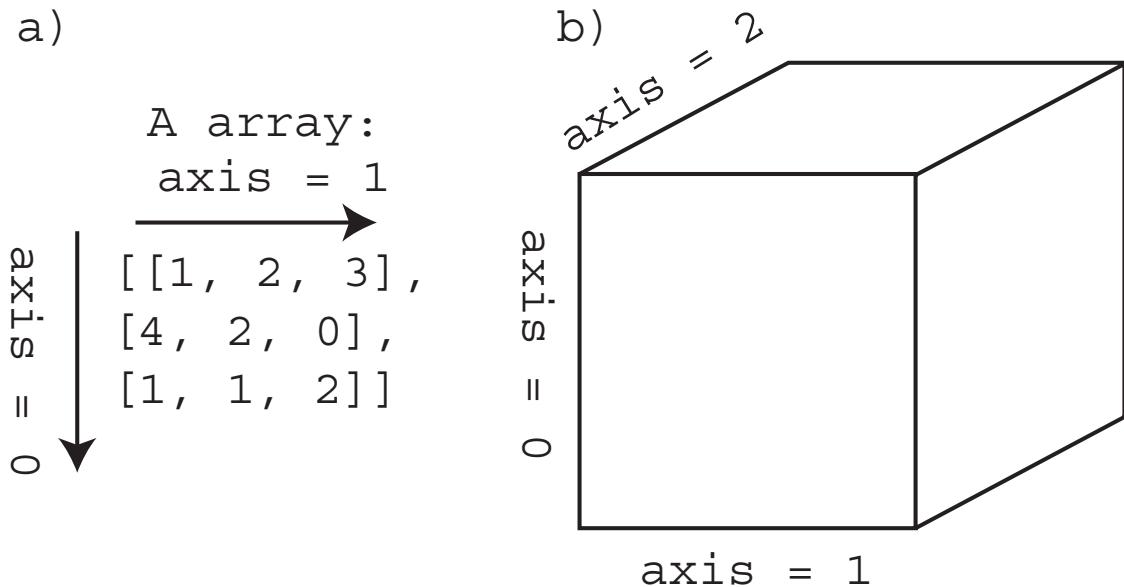
Let's see what the methods can do. First, arrays made in the above example are of different data types. To find out what data type an array is, just use the method `dtype` as in:

```

>>> D.dtype
dtype('float64')
>>>

```

And of course arrays, unlike lists have dimensions and shape. Dimensions tell us how many axes there are with axes defined as in this illustration:



As shown above our **A** array has two dimensions (axis 0 and 1). To get Python to tell us this, we use the **ndim** method:

```
>>> A= numpy.array([[1,2,3],[4,2,0],[1,1,2]]) # just to remind you  
>>> A.ndim  
2
```

Notice how **zeros**, **ones** and **ndarray** used a shape tuple in order to define the arrays in the examples above. The shape of an array is how many elements are along each axis. So, naturally we see that the C array is a 2x3 array. Python returns a tuple with the shape information using the **shape** method:

```
>>> C.shape  
(2, 3)
```

Let's say we don't want a 2x3 array for the sequence in the array **C**, but we want a 3x2 array. Python can reshape an array with a different shape tuple like this:

```
>>> C.reshape((3,2))  
array([[1, 2],  
       [3, 4],  
       [5, 6]])
```

And sometimes we just want all the elements lined up along one axis. We could do that with `reshape` of course using a tuple with the size of the array (the total number of elements). You can see that this is 6 here. We could even get python to tell us what the size is (`C.size`) and use that in the reshape size tuple. Alternatively we can use the `ravel()` method which doesn't require us to know the size in advance:

```
>>> C.ravel()
array([1, 2, 3, 4, 5, 6])
```

There are other ways to reshape, slice and dice arrays. The syntax for slicing of arrays is similar to that for lists:

```
>>> B=A[0:2] # carve the top two lines off of matrix A from above
array([[1, 2, 3],
       [4, 5, 6]])
```

Lots of applications in Earth Science require the transpose of an array:

```
>>> A.transpose() # this is the same as A.T
array([[1, 4, 7],
       [2, 5, 8],
       [3, 6, 9]])
```

Also, we can concatenate two arrays together with the - you guessed it - `concatenate()` method. For a lot more tricks with arrays, go to the NumPy Reference website here: <http://docs.scipy.org/doc/numpy/reference/>.

To convert the `A` array to a list: `L=A.tolist()`, from a list or tuple to an array: `A=numpy.array(L)`, or from a list, a tuple or an array to a NumPy array: `a=numpy.asarray(L)`

Let's go a bit deeper into slicing of arrays. First a review of lists. You will recall that in python, indexing starts with 0, so for the list `L=[0,2,4,6,8]`, `L[1]` is 2. The index of the last item is -1, so `L[-1]=8`. To find out what the index for the number 4 is, for example, we have the `index()` method: `L.index(4)`, which will return the number 2. We actually already used this method when we implemented command line arguments, but it wasn't really explained. We know that to reassign a given index a new value we use the syntax `L[1]=2.5`. And to use a part of a list (a slice) we use, e.g., `B=L[2:4]`, which defines `B` as a list with `L`'s elements 2 and 3 (4 and 6). And you also know that `B=L[2:]` takes all the elements from 2 to the end. From these

examples, you can infer that the basic syntax for slicing is [start:stop:step]; if the step is omitted it is assumed to be 1.

Arrays (and matrices) work in a similar fashion to lists, but these are multidimensional objects, so things get hairy fast. The basic syntax is the same: [start:stop:step], or i:j:k. but with Python arrays, we step through all the j's for each i at step k. This is best shown with examples:

```
>>> import numpy
>>> A=numpy.linspace(0,29,30)
>>> B=A.reshape(5,6)
array([[ 0.,  1.,  2.,  3.,  4.,  5.],
       [ 6.,  7.,  8.,  9., 10., 11.],
       [12., 13., 14., 15., 16., 17.],
       [18., 19., 20., 21., 22., 23.],
       [24., 25., 26., 27., 28., 29.]])
>>> B[1:3,:-1:2]
array([[ 6.,  8., 10.],
       [12., 14., 16.]])
```

Let's pick about the statement B[1:3,:-1:2] to see if we can understand what it does. The first part alone returns lines 2 and 3:

```
>>> B[1:3]
array([[ 6.,  7.,  8.,  9., 10., 11.],
       [12., 13., 14., 15., 16., 17.]])
```

Here j goes from [-1], in other words, we all but the last element:

```
>>> B[1:3,:-1]
array([[ 6.,  7.,  8.,  9., 10.],
       [12., 13., 14., 15., 16.]])
```

And finally, we have the step of 2, which takes every other element:

```
>>> B[1:3,:-1:2]
array([[ 6.,  8., 10.],
       [12., 14., 16.]])
```

For more on array slicing (indexing), see:

<http://docs.scipy.org/doc/numpy/reference/arrays.indexing.html>

7.4 Pandas

Now that you have fallen in love with Python and Numpy, we have a new treat for you: pandas. Pandas is a powerful module available with the Python distribution that you should have installed in the Installing PmagPy section. It supports elegant data structures and tools for wrangling the data which allow fast and user-friendly data analysis. There are two basic data structures: the Series (a one-dimensional array like object that is a data array with an associated array of indices which can be numbers or text) and the DataFrame (a spreadsheet like data table).

First, invoke pandas by importing it, then create some data Series using several approaches:

```
>>> import pandas
>>> obj = pandas.Series([1,2,3,4]) # create first pandas object with numeric index
>>> obj
0    1
1    2
2    3
3    4
dtype: int64
>>> obj2=pandas.Series([1,2,3,4],index=['a','b','c','d']) # create second pandas object with categorical index
>>> obj2
a    1
b    2
c    3
d    4
dtype: int64
>>> TelNos={'lisa':46084,'lab':46531,'jeff':44707} # create a dictionary
>>> obj3=pandas.Series(TelNos) # create a pandas Series from the dictionary.
>>> obj3
jeff    44707
lab     46531
lisa    46084
dtype: int64
```

Another very useful pandas object is the DataFrame. These have both row and column indices and are like a dictionary of Series so are much more flexible than the Numpy array objects. Here is an example:

```
>>> data={'telnos':['44707','46531','46084'],
```

```
...      'names':[‘jeff’,‘lisa’,‘lab’],  
...      ‘rooms’: [‘300D RH’,‘300E RH’,‘1162 SvH’]}  
>>> frame=pandas.DataFrame(data)  
>>> frame  
   names      rooms telnos  
0 jeff      300D RH  44707  
1 lisa      300E RH  46531  
2 lab       1162 SvH  46084
```

There are many methods associated with pandas objects which allow searching, massaging and generally fiddling with the data. You should check out some of the many tutorials on pandas on the web.

7.5 Python Scripts

Are you tired of typing yet? Python scripts are programs that can be run and re-run from the command line. You can type in the same stuff you've been doing interactively into a script file (ending in .py). You can edit scripts with your favorite text editor (NOT Word!). And then you can run them like this:

```
%python < myscript.py
```

On a Mac or Unix system, you can put in a header line identifying the script as python (`#!/usr/bin/env python`), make it executable (`chmod a+x`) and run it like this:

```
$ myscript.py
```

On PCs, you can just type the name of the script without the header or the chmod command. But, because PCs don't come standard with a **cat** command, you have to create the file with Notepad, instead of with **cat** for all the examples using **cat**.

Here is an example that creates a script using the Unix **cat** command, makes it executable and then runs it:

```
$ cat > printmess.py  
#!/usr/bin/env python  
# simple Python test program (printmess.py)
```

```

print 'test message'
^-D
$ chmod a+x printmess.py
$ ./printmess.py
test message

```

In a Python script on Unix machines (including MacOS), the first line MUST be:

```
#! /usr/bin/env python
```

so that the file is interpreted as Python. Unlike Fortran or C, you CANNOT start with a comment line (try switching lines 1 and 2 and see what happens).

The second line is a comment line. Anything to the right of # is assumed to be a comment. Notice that print goes by default to your screen. Because the message is a string, you can use single or double quotes for the test message. You can get an apostrophe in your output by using double quotes and quote marks by using single quotes, i.e.,

```

#! /usr/bin/env python
# simple Python test program 2 (printmess2.py)
print "The pump don't work 'cuz the vandals took the handles"
print 'She said "I know what it\'s like to be dead"'

```

produces:

```

$ ./printmess2.py
The pump don't work 'cuz the vandals took the handles
She said "I know what it's like to be dead"
%

```

In the second print statement, the \' is necessary to prevent an error (try it). This is an example of a Python ‘escape code’. These are used to escape some special meaning, as in an end-quote for a string in this example. We use the backslash to say that we really really want a quote mark here. Other escape codes are listed here:

<http://www.python-course.eu/variables.php>

Here’s another example of a program - this one has an typo in line 4:

```

#! /usr/bin/env python
abeg = 2.1

```

```
aend = 3.9
adif = aend - abge
print 'adif = ', adif
```

You had intended to type 'abeg' but typed 'abge' instead. When you run the program, you get an error message:

```
Traceback (most recent call last):
  File './undeclared.py', line 4, in <module>
    adif = aend - abge
NameError: name 'abge' is not defined
```

Error messages are a desirable feature of Python. You don't want the program to run by assigning some arbitrary value to abge and giving you a wrong answer. Yet many languages will do exactly that.

7.6 Code blocks

Any reasonable programming language must provide a way to group blocks of code together, to be executed under certain conditions. In Fortran, for example, there are if statements and do loops which are bounded by the statements if, endif and do, endo respectively. Many of these programs encourage the use of indentation to make the code more readable, but do not require it. In Python, indentation is the way that code blocks are defined - there are no terminating statements. Also, the initiating statement terminates in a colon. The trick is that all code indented the same number of spaces (or tabs) to the right belong together. The code block terminates when the next line is less indented. A typical Python program looks like this:

```
program statement
block 1 top statement:
    block 1 statement
    block 1 statement \
        ha-ha i can break the indentation convention!
    block 1 statement
block 2 top statement:
    block 2 statement
    block 2 statement
block 3 top statement:
```

```

block 3 statement
block 3 statement
block 4 top statement: block 4 single line of code
block 2 statement
block 2 statement
block 1 statement
block 1 statement
program statement

```

Exceptions to the code indentation rules are:

- Any statement can be continued on the next line with the continuation character \ and the indentation of the following line is arbitrary.
- If a code block consists of a single statement, then that may be placed on the same line as the colon.
- The command `break` breaks you out of the code block. Use with caution!
- There is a cheat that comes in handy when you are writing a complicated program and want to put in the code blocks but don't want them to DO anything yet: the command `pass` does nothing and can be used to stand in for a code block.

Good housekeeping Tip #2: Always use only spaces or only tabs in your code indentation. We use only spaces because we use vi to write my code. Others use Xcode, the Python IDLE program, or TextWrangler to write their code and some of these things use tabs by default. Whatever you do BE CONSISTENT because tabs are not the same as spaces in Python even if you can't tell the difference just by looking at it.

In the following, I'll show you how Python uses code blocks to create "do" and "while" loops, and "if" statements.

The for loop

Looping through lists

Here is an example of a simple "for loop":

```

#!/usr/bin/env python
mylist=[42,'spam','ocelot']
for i in range(0,len(mylist),1): # note absence of Indices list, start and step

```

```
print mylist[i]
print 'All done'
```

This script creates the list `mylist` with the line `mylist=[42,'spam','ocelot']`. The length of `mylist` is an integer value returned by `len(mylist)`. The script uses this integer as the ‘stop’ value in the `range()` function, which returns a list of integers from 0 to the stop value MINUS ONE at intervals of one. [The minus one convention is hard to get use to for Fortran programmers, but it is typical of Python syntax (and also of C) so just deal with it.] Anyway, `range(start,stop,step)` is just like `numpy.arange(start,stop,step)` but returns integers instead of floats. Also, like `numpy.arange()`, there is a short hand form when the minimum is zero and the interval is one, so we could (and will) just use the command `range(stop)`.

Python makes i step through the list of numbers from 0 to 2, printing the i^{th} element of `mylist`. Note how the print command is indented - this is the program block that is executed for each i . Note also that the line could have been on the previous line after the colon, because there is only one line in the program block. But never-mind, this way works too. When i finishes its business, the program block terminates. At that point, the program prints out the ‘All done’ string. There is no “enddo” statement or equivalent in Python.

But, Python is far more fun than the old-school `for i in` syntax in the above code snippet. In Python we can just step through a list directly. Here is another script which does just that (why not?):

```
#!/usr/bin/env python
mylist=[42,'spam','ocelot']
for item in mylist: # note absence of range statement
    print item
print 'All done'
```

Note that of course we could have used any variable name instead of ‘item’, but it makes sense to use variable names that mean what they do. It is easier to understand what ‘item’ stands for than just the Fortran style of i .

Here is an example with a little more heft to it. It creates a table of trigonometry functions, spitting them out with a formatted print statement:

```
#! /usr/bin/env python
import numpy as np
deg2rad = np.pi/180. # remember conversion to radians
```

```

for theta in range(90): # short form of range, returns [0,1,2...89]
    ctheta = np.cos(theta*deg2rad) # define ctheta as cosine of theta
    stheta = np.sin(theta*deg2rad)# define stheta as sine of theta
    ttheta = np.tan(theta*deg2rad) # define ttheta as tangent of theta
    print '%5.1f %8.4f %8.4f %8.4f' %(theta, ctheta, stheta, ttheta)

```

Let's pick this one apart a bit. First, notice the use of the variable `deg2rad` to convert from degrees to radians. Also notice how `deg2rad` is defined: `deg2rad = np.pi/180.` using the `NumPy` function for π and the decimal point after 180. While in this case, it makes absolutely no difference (try it!), it is a good practice to use real numbers if you want your variable to stay real. In fact:

Good housekeeping Tip #3: Always use a decimal if you want your variable to be a floating point variable.

The expression `ctheta = np.cos(theta*deg2rad)` uses the `numpy` cosine function. Ideally `theta` should be a real variable while in fact it is an integer in this expression, but fortunately Python figures that out and converts it to a real. Note that we could have also converted theta to a float first with the command `float(theta)`.

```
print '%5.1f %8.4f %8.4f %8.4f' %(theta, ctheta, stheta, ttheta)
```

To make the output look nice, we do not use

```
print theta, ctheta, stheta, ttheta
```

which would space the numbers irregularly among the columns and put out really long numbers. Instead, we explicitly specify the output format. The output format is given in the quotes. The format for each number follows the `%`, `5.1f` is for 5 spaces of floating point output, with 1 space to the right of the decimal point. The single blank space between `%5.1f` and `%8.4f` is included in the output, in fact any text there is reproduced exactly in the output, thus to put commas between the output numbers, write:

```
print '%5.1f, %8.4f, %8.4f, %8.4f' %(theta, ctheta, stheta, ttheta)
```

Tabs (`\t`) would be formatted like this:

```
print '%5.1f \t %8.4f\t %8.4f,\t %8.4f' %(theta, ctheta, stheta, ttheta)
```

Looping through arrays

We just learned that `for` loops with lists just step through item by item. In n-dimensional arrays, they steps through row by row (like in slicing). For example,

```
>>> for r in B:  
...     print r  
...  
[ 0.  1.  2.  3.  4.  5.]  
[ 6.  7.  8.  9.  10. 11.]  
[ 12. 13. 14. 15. 16. 17.]  
[ 18. 19. 20. 21. 22. 23.]  
[ 24. 25. 26. 27. 28. 29.]
```

If you really want to step through element by element, you can use the `ravel()` method which flattens an N-dimensional array to a single dimension:

```
>>> for e in B.ravel():  
...     print e  
...  
0.0  
1.0  
2.0  
3.0  
etc.
```

For more on looping (or iterating), see:

<http://docs.scipy.org/doc/numpy/reference/arrays.nditer.html>

If and while blocks

The “for loop” is just one way of controlling flow in Python. There are also `if` and `while` code blocks. These execute code blocks the same way as for loops (colon terminated top statements, indented text, etc.). For both of these, the code block is executed if the top statement is TRUE. For the “if” block, the code is executed once but in a “while” block, the code keeps executing as long as the statement remains TRUE.

The key to flow control therefore is in the top statement of each code block; if it is TRUE, then execute, otherwise skip it. To decide if something is TRUE or not (in the boolean sense), we need to evaluate a statement using

comparisons. Here's a handy table with comparisons (relational operators) in different languages:

Comparisons						
F 77	F90	C	MATLAB	PYTHON	meaning	
.eq.	==	==	==	==	equals	
.ne.	/=	!=	~=	!=	does not equal	
.lt.	<	<	<	<	less than	
.le.	<=	<=	<=	<=	less than or equal to	
.gt.	>	>	>	>	greater than	
.ge.	>=	>=	>=	>=	greater than or equal to	
.and.	.and.	&		&	and	
.or.	.or.	—	—	or		

These operators can be combined to make complex tests. Here is a juicy complicated statement:

```
if ( (a > b and c <= 0) or d == 0):
    code block
```

There are rules for the order of operations for these things like, multiplication gets done before addition. But these are easy to forget. You can look it up in the documentation if you are unsure or, better, just put in enough parenthesis to make it completely clear to anyone reading your code.

Good housekeeping Tip #4: Use parentheses liberally - make the order of operation completely unambiguous even if you could get away with fewer.

One nice aspect of Python compared to C is that if you make a mistake and type, for example,

```
if (a = 0):
```

you will get an error message during compilation. In C this is a valid statement with a completely different meaning than is intended!

Finer points of ‘if’ blocks

The simplest ‘if’ block works just like we have described:

```
if (2+2)==4: # note the use of '==' and parentheses in comparison statement
    print 'I can put two and two together!'
```

However, as in any other reasonable programming language, there are whistles and bells to the ‘if’ code blocks. In Python these are: `elif` and `else`. A code block gets executed if the top `if` statement is FALSE and the `elif` statement is TRUE. If both the top `if` and the `elif` statements are FALSE but the `else` statement is TRUE, then Python will execute the block following the `else`. Consider these examples:

```
#!/usr/bin/env python
mylist=['jane','doug','denise']
if 'susie' in mylist:
    pass # don't do anything
if 'susie' not in mylist:
    print 'call susie and apologize!'
    mylist.append('susie')
elif 'george' in mylist: # if first statement is false, try this one
    print 'susie and george both in list'
else: # if both statements are false, do this:
    print "susie in list but george isn't"
```

While loops

As already mentioned, the ‘while’ block continues executing as long as the `while` top statement is TRUE. In other words, the `if` block is only executed once, while the `while` block keeps looping until the statement turns FALSE. Here are a few examples:

```
#!/usr/bin/env python
a=1
while a < 10:
    print a
    a+=1
print "I'm done counting!"
```

Code blocks in interactive Python

All of these program blocks can also be done in an interactive session also using indentation. The interactive shell responds with ‘.....’ instead of ‘>>>’ once you type a statement it recognizes as a top statement. To signal that you are done with the program block, simply hit return:

```
>>> a=1
>>> while a<10:
....    print a
....    a+=1
....[return to execute block]
```

7.7 File I/O in Python

Python would be no better than a rather awkward graphing calculator (and we haven't even gotten to the graphing part yet) if we couldn't read data in and spit data out. You learned a rudimentary way of spitting stuff out already using the `print` statement, but there is a lot more to file I/O in Python. We would like to be able to read in a variety of file formats and output the data any way we want. In the following we will explore some of the more useful I/O options in Python.

Reading data in

From a file

If you are using Python interactively or want interactivity in a script, use the command: `raw_input()`. It acts as a prompt and reads in whatever is supplied prior to a return as a string.

```
X=[] # make a list to put the data in
ans=float(raw_input("Input numeric value for X: "))
X.append(ans) # append the value to X
print X[-1] # print the last item in the list
```

In this example, the variable `ans` will be read in as a string variable, converted to a float and appended to the list, `X`. `raw_input()` is a simple but rather annoying way to enter things into a program. Another (less annoying) way is put the data in a file (e.g., `myfile.txt`) with cat, paste, Excel (saved as a text file), or whatever and read it into Python. The procedure is straight-forward: we must first open the file, then read it in and parse lines into the desired variables.

To open a file we use the command `open()`, one of Python's built-in functions. For a complete list of these, see:

<http://docs.python.org/library/functions.html>

The `open()` function returns an object, complete with methods, like `readlines()` which, yes, reads all the lines. Suppose you have a file containing the coordinates of some seismic stations which you want to plot on a map or something. (In fact, it is in the `data_files/LearningPython` directory. The file is called `station.list` and its first five lines are:

```
9.02920 38.76560 2442 AAE
42.63900 74.49400 1645 AAK
37.93040 58.11890 678 ABKT
51.88370 -176.68440 116 ADK
-13.90930 -171.77730 706 AFI
```

Here is a script (`ReadStations.py`) that will open a file `station.list`, read in the data and print it out line by line.

```
#!/usr/bin/env python
f=open('station.list')
StationNFO=f.readlines()
for line in StationNFO:
    print line
```

If you run this script, you will get this behavior:

```
$ ReadStations.py
9.02920 38.76560 2442 AAE

42.63900 74.49400 1645 AAK

37.93040 58.11890 678 ABKT

51.88370 -176.68440 116 ADK
etc.
```

The function `open()` has some bells and whistles to it and has the form `open(name[, mode[, buffering]])` where the stuff in square brackets is optional. The ‘name’ argument is the file name to open and ‘mode’ is the way in which it should be opened, most commonly for reading ‘r’, writing ‘w’ or appending ‘a’. We use the form ‘rU’ for unformatted reading because we often want to read in files that were saved in Dos, Mac OR Unix line endings and ‘rU’ figures all that out for you. Just in case you are curious, Unix lines end in

'\n', Mac files in '\r' and Dos (and windows) lines end in '\r\n'. we never use the 'buffering' argument and don't know what it does.

If you are curious about the line endings, try typing out the 'representation' of the line `repr(line)` in the above script and you get all the stuff that is normally invisible like the apostrophes and the line terminations:

```
$ ReadStations.py
' 9.02920 38.76560 2442 AAE \n'
' 42.63900 74.49400 1645 AAK \n'
' 37.93040 58.11890 678 ABKT\n'
' 51.88370 -176.68440 116 ADK \n'
' -13.90930 -171.77730 706 AFI \n'
etc.
```

Notice how in our first version, printing the line also printed the line feed (\n) as an extra line. To clean this off of each line, we can use the string `strip()` function:

```
print line.strip('\n')
```

Putting this into the code results in this behavior:

```
$ ReadStations.py
9.02920 38.76560 2442 AAE
42.63900 74.49400 1645 AAK
37.93040 58.11890 678 ABKT
```

Let's say you want to read in the data table into lists called Lats, Lons, and StaIDs (the first three columns). You need to split each line into its columns and append the correct column into the appropriate list. Some languages automatically split on the spaces but Python reads in the entire line as a string and ignores the spaces or other possible delimiters (commas, semi-colons, tabs, etc.). To split the line, we use the string function `split([sep])` where `[sep]` is an optional separator. If no separator is specified (e.g., `line.split()`), it will split on spaces. Anything could be a separator, but the most common ones are ',', ';', and '\t'. The latter is how a tab appears if you were to, say, print out the representation of the line, which shows all the invisibles.

Here is a slightly modified version of `ReadStations.py`, `ParseStations.py` which parses out the lines and puts numbers (floats or integers) in the right lists:

```
#!/usr/bin/env python
Lats,Lons,StaIDs,StaName=[],[],[],[]# creates lists to put things in
StationNFO=open('station.list').readlines() # combines the open and readlines methods!
for line in StationNFO:
    nfo=line.strip('\n').split() # strips off the line ending and splits on spaces
    Lats.append(float(nfo[0])) # puts float of 1st column into Lats
    Lons.append(float(nfo[1]))# puts float of 2nd column into Lons
    StaIDs.append(int(nfo[2])) # puts integer of 3rd column into StaIDs
    StaName.append(nfo[3])# puts the ID string into StaName
    print Lats[-1],Lons[-1],StaIDs[-1] # prints out last thing appended
```

From Standard Input

Python can also read from standard input. To do this, we need a system specific module, called `sys` which among other things has a `stdin` method. So, instead of specifying a file name in the `open` command, we could substitute the following line:

```
#!/usr/bin/env python
import sys
Lats,Lons,StaIDs,StaName=[],[],[],[]# creates lists to put things in
StationNFO=sys.stdin.readlines() # reads from standard input
for line in StationNFO:
    nfo=line.strip('\n').split() # strips off the line ending and splits on spaces
    Lats.append(float(nfo[0])) # puts float of 1st column into Lats
    Lons.append(float(nfo[1]))# puts float of 2nd column into Lons
    StaIDs.append(int(nfo[2])) # puts integer of 3rd column into StaIDs
    StaName.append(nfo[3])# puts the ID string into StaName
    print Lats[-1],Lons[-1],StaIDs[-1] # prints out last thing appended
```

The program can be invoked with:

```
$ ReadStations.py < station.list
```

We could also use command line switches by reading in arguments from the command line. In the following example, we use the switch '`-f`' with the following argument begin the file name:

Command line switches

```
#!/usr/bin/env python
import sys
Lats,Lons,StaIDs,StaName=[],[],[],[]# creates lists to put things in
if '-f' in sys.argv: # look in list of command line arguments
    file=sys.argv[sys.argv.index('-f')+1] # find index of '-f' and increment by 1
StationNFO=open(file,'rU').readlines() # open file
for line in StationNFO:
    nfo=line.strip('\n').split() # strips off the line ending and splits on space
    Lats.append(float(nfo[0])) # puts float of 1st column into Lats
    Lons.append(float(nfo[1]))# puts float of 2nd column into Lons
    StaIDs.append(int(nfo[2])) # puts integer of 3rd column into StaIDs
    StaName.append(nfo[3])# puts the ID string into StaName
    print Lats[-1],Lons[-1],StaIDs[-1] # prints out last thing appended
```

This version can be invoked with:

```
$ ReadStations.py -f station.list
```

Reading numeric files

In the special case where the data in a file are entirely numeric, you can read in the file with a special `numpy` function `loadtxt()`. This reads the data into a list whereby each element of the list is a list of numbers from each line.

Writing data out

Let's say we have a Python module that will convert latitudes and longitudes to UTM coordinates. O.K. We really do have one that we downloaded from here:

<http://code.google.com/p/pyproj/issues/attachmentText?id=27&aid=-808841747718>

We wrote a script (`ConvertStations.py`) to convert each of the stations in my list to their UTM equivalents (assuming these were in a WGS-84 ellipsoid). It would be nice if after having done this to the data, we could then write it out somehow, preferably to a file. Of course we could use the `print` command like this:

```
#!/usr/bin/env python
import UTM # imports the UTM module
Ellipsoid=23-1 # UTMs code for WGS-84
```

```

StationNFO=open('station.list').readlines()
for line in StationNFO:
    nfo=line.strip('\n').split()
    lat=float(nfo[0])
    lon=float(nfo[1])
    StaName= nfo[3]
    Zone,Easting, Northing=UTM.LLtoUTM(Ellipsoid,lon,lat)
    print StaName, ': ', Easting, Northing, Zone

```

which spits out something like this:

```

$ ConvertStations.py
AAE : 474238.170087 998088.469113 37P
AAK : 458516.115522 4720850.45385 43T
ABKT : 598330.712671 4198681.92944 40S
ADK : 521722.179764 5748148.625 1U
AFI : 416023.683618 8462168.07766 2L
etc.

```

I could save the output with a UNIX re-direct:

```
ConvertStations.py > mynewfile
```

But we yearn for more. So, more elegantly, we can open an output file [for appending 'a' or (over)writing 'w'] write a formatted string using the write method on the output file object with format string:

```

#!/usr/bin/env python
import UTM # imports the UTM module
outfile=open('mynewfile','w') # creates outfile object
Ellipsoid=23-1 # UTMs code for WGS-84
StationNFO=open('station.list').readlines()
for line in StationNFO:
    nfo=line.strip('\n').split()
    lat=float(nfo[0])
    lon=float(nfo[1])
    StaName= nfo[3]
    Zone,Easting, Northing=UTM.LLtoUTM(Ellipsoid,lon,lat)
    outfile.write('%s %s %s %s\n'%(StaName, Easting, Northing, Zone))

```

The only significant changes are 1) the object `outfile` is opened for writing. Note that this will clobber anything in a pre-existing file by that name and 2) the output file gets written to in the statement with a write method on the output file object:

```
outfile.write('%s %s %s %s\n'%(StaName, Easting, Northing, Zone))
```

The write statement uses the syntax: 'format string' %(list of variables tuple). Format strings have these rules:

- For each variable in (what you...) you need a format: %s for string, %i for integer, %f for float, %e for exponent
- you can also specify further, e.g.: %7.1f for 7 characters with 1 after the decimal %10.3e for 10 characters with 3 after the decimal
- where the number of characters include the decimal and padded spaces
- As noted before, the format string can include punctuation:

```
x,y=4.82,2.3e3
print '%.1f,%s\t%.3e'%(x,'hi there',y)
4.8,hi there 2.300e+03
```

- In the `ConvertStations2.py` script, the '\n' string puts a UNIX line ending on it. Without that, the whole file is but a single line (very annoying).

A session using the script (`ConvertStations2.py` and a peek at the resulting file could look like this:

```
$ ConvertStations2.py
$ head mynewfile
AAE 474238.170087 998088.469113 37P
AAK 458516.115522 4720850.45385 43T
ABKT 598330.712671 4198681.92944 40S
ADK 521722.179764 5748148.625 1U
AFI 416023.683618 8462168.07766 2L
ALE 509467.666259 9161062.29194 20X
ALQ 366981.843985 3868044.56906 13S
ANMO 366981.843985 3868044.56906 13S
ANTO 482347.254856 4413225.7807 36S
AQU 368638.770654 4690300.1797 33T
```

The Unix `head` command types out the first 10 lines of a file but has no DOS equivalent.

7.8 Functions

So far you have learned how to use functions from program modules like [NumPy](#). You can imagine that there are many bits of code that you might write that you will want to use again and again, say converting between degrees and radians and back, or finding the great circle distance between two points on Earth, or converting between UTM and latitude/longitude coordinates (as in [UTM.py](#), my new favorite package). The basic structure of a program with a Python function is:

```
#!/usr/bin/env python

def FUNCNAME(in_args):
    """
    DOC STRING
    """
    some code that the functions does something
    return out_args

FUNCNAME(in_args) # this calls the function
```

Line by line analysis

```
def FUNCNAME(in_args):
```

The first line must have 'def' as the first three letters, must have a function name with parentheses and a terminal colon. If you want to pass some variables to the function, they go where in_arg sits, separated by commas. There are no output variables here.

There are four different ways to handle argument passing.

- 1) You could have a function that doesn't need any arguments at all:

```
#!/usr/bin/env python
def gimmelpi():
    """
    """
    returns pi
    """
```

```
        return 3.141592653589793
print gimpipi()
```

- 2) You could use a set list of what are called ‘formal’ variables that must be passed:

```
#!/usr/bin/env python
def deg2rad(degrees):
    """
    converts degrees to radians
    """
    return degrees*3.141592653589793/180.
print '42 degrees in radians is: ',deg2rad(42.)
```

- 3) You could have a more flexible need for variables. You signal this by putting *args in the in_args list (along with any formal variables you want):

```
#!/usr/bin/env python
def print_args(*args):
    """
    prints argument list
    """
    print 'You sent me these arguments: '
    for arg in args:
        print arg
print_args(1,4,'hi there')
print_args(42)
```

- 4) You can use a keyworded, variable-length list by putting **kwargs in for in_args:

```
#!/usr/bin/env python
def print_kwargs(**kwargs):
    """
    prints keyworded argument list
    """
    for key in kwargs:
        print '%s %s' %(key, kwargs[key])

print_kwargs(arg1='one',arg2=42,arg3='ocelot')
```

Doc String

Although you can certainly write functional code without a document string, make a habit of always including one. Trust me - you'll be glad you did. This can later be used to remind you of what you thought you were doing years later. It can be used to print out a help message by the calling program and it also let's others know what you intended. Notice the use of the triple quotes before and after the documentation string - that means that you can write as many lines as you want.

Function body

This part of the code must be indented, just like in a for loop, or other block of code.

Return statement

You don't need this unless you want to pass back information to the calling body (see, for example `print_kwargs()` above). Python separates the entrance and the exit. See how it can be done in the `gimme_pi()` example above.

Main program as function

It is considered good Python style to treat your main program block as a function too. (This helps with using the document string as a help function and building program documentation in general.) In any case, we recommend that you just start doing it that way too. In this case, we have to call the main program with the final (not indented) line `main()`:

```
#!/usr/bin/env python
def print_kwargs(**kwargs):
    """
    prints keyworded argument list
    """
    for key in kwargs:
        print '%s %s' %(key, kwargs[key])

def main():
    """
    calls function print_kwargs
```

```

    """
print_kwargs(arg1='one',arg2=42,arg3='ocelot')
main() # runs the main program

```

Notice how in the above examples, all the functions preceded the main function. This is because Python is an interpreter and not compiled - so it won't know about anything declared below as it goes through the script line by line. On the other hand, we've been running lots of functions and they were not in the program we used to call them. The trick here is that you can put a bunch of functions in a separate file (in your path) and import it, just like we did with [NumPy](#). Your functions can then be called from within your program in the same way as for [NumPy](#).

So let's say we put all the above functions in a file called `myfuncs.py`:

```

def gimmepi():
    """
    returns pi
    """
    return 3.141592653589793
def deg2rad(degrees):
    """
    converts degrees to radians
    """
    return degrees*3.141592653589793/180.
def print_args(*args):
    """
    prints argument list
    """
    print 'You sent me these arguments: '
    for arg in args:
        print arg

```

We could then just import the module `myfuncs` from within another program, or just interactively. We can use the functions, or just call for help:

```

$ python
>>> import myfuncs
>>> print myfuncs.gimmepi()
3.14159265359
>>> print myfuncs.print_args.__doc__

```

```
prints argument list  
>>>
```

Scope of variables

Inside a function, variable names have their own meaning which in many cases will be different from inside the calling function. So, variables names declared inside a function stay in the function. This is true unless you declare them to be “global”. Here is an example in which the main program “knows” about the functions variable `V`:

```
def myfunc():  
    global V  
    V=123  
def main():  
    myfunc()  
    print V  
main()
```

In addition to being able to write your own functions, of course Python has LOTS of modules and a gazzillion functions. The enthought distribution that you are using Includes plotting, numerical recipes, trig functions, image manipulation, animation, and many more.

7.9 Classes

Before we go any further, we need to learn some basic concepts about classes. These are the basis of “object oriented programming” OOP (that again!). Class objects lie behind plotting, for example and a rudimentary understanding of what they are and how they work will come in handy when we start doing anything but the simplest plotting exercises.

A class object is created by a call to a “class definition” which which can be thought of as a blueprint for the class object. Here is an simple example of a class definition:

```
class Circle:  
    ....
```

```
This is simple example of a class
#####
pi=3.141592653589793
def __init__(self,r):
    self.r=r
def area(self):
    return 0.5*self.pi*self.r**2
def circumference(self):
    return 2.*pi*self.r
```

Saving this class in a file called `Shapes.py` we can use it in a Python session in a manner similar to function modules:

```
>>> import Shapes # import the class
>>> r=4.0
>>> C=Shapes.Circle(r) # create a class instance with r=4.
>>> C.pi # retrieve an attribute
3.141592653589793
>>> C.area() # retrieve a method
25.132741228718345
>>> C.r=2.0 # change the value of r
>>> C.area() # get a new area
6.283185307179586
```

In spite of superficial similarities, classes are not the same as functions. Although the Shape module is imported just the same as any other, to use it, we first have to create a class “instance” (`C=Shapes.Circle(r)`). `C` is an object with “attributes” (variables) and “methods”. All methods (parts that start with “def”), have an argument list. The first argument has to be a reference to the class instance itself, or “self”, followed by any variables you want to pass into the method. So the `__init__` method initializes the instance attributes of an object. In the above case, it defined the attribute `r`, which gets passed in when the class is first called. Asking for any attribute (note the lack of parentheses), retrieves the current value of that attribute. Attributes can be changed (as in `C.r=2.0`).

The other methods (`area` and `circumference`) are defined like any function except note the use of ‘self’ as the first argument. This is required in all class method definitions. In our case, no other parameters are passed in because the only one used is `r`, so the argument list consists of only `self`. Calling these methods returns the current values of these methods.

You can make a subclass (child) of the parent class which has all the attributes and methods of the parent, but may have a few attributes and methods of its own. You do this by setting up another class definition within a class.

So, the bottom line about classes is that they are in the same category of things as variables, lists, dictionaries, etc. That is, they are ‘data structures’ - they hold data, and the methods to process that data. If you are curious about classes, there’s lots more to know about classes that we don’t have time to get into, but you can find useful tutorials online:

(e.g., <http://www.sthurlow.com/python/lesson08/>)

7.10 Matplotlib

So far you have learned the basics of Python, and NumPy. But Python was sold as a way of visualizing data and we haven’t yet seen a single plot (except a stupid one in the beginning). There are many plotting options within the Python umbrella. The most mature and the one we are most familiar with is [matplotlib](#), a popular graphics module of Python. Actually [matplotlib](#) is a collection of a bunch of other modules, toolkits, methods and classes. For a fairly complete and readable tour of matplotlib, check out these links:

<http://matplotlib.sourceforge.net/Matplotlib.pdf>

and here:

<http://matplotlib.sourceforge.net/>

A first plot

Let’s start by reviewing the simple plot script ([matplotlib1.py](#)):

```
#!/usr/bin/env python
import matplotlib
matplotlib.use('TkAgg') # my favorite backend
import pylab # module with matplotlib
pylab.plot([1,2,3]) # plot some numbers
pylab.ylabel('Y') # label the y-axis
pylab.show() # reveal the plot
```

The first step should be obvious by now, it imports [matplotlib](#). Figures are rendered on “backends” so they appear on screen. There are a lot of different back-ends with slightly different looks. Some work better on different operating systems. We use the very old school backend called

“TkAgg” backend because it “works”. So step 2 sets the backend: `matplotlib.use("TkAgg")`. The module `matplotlib` itself contains a lot of other modules. One of these, `pylab` is the “business end” that has a lot of plotting methods and classes. It must be loaded alongside `matplotlib`, so step 3 is: `import pylab`. After that the fun starts.

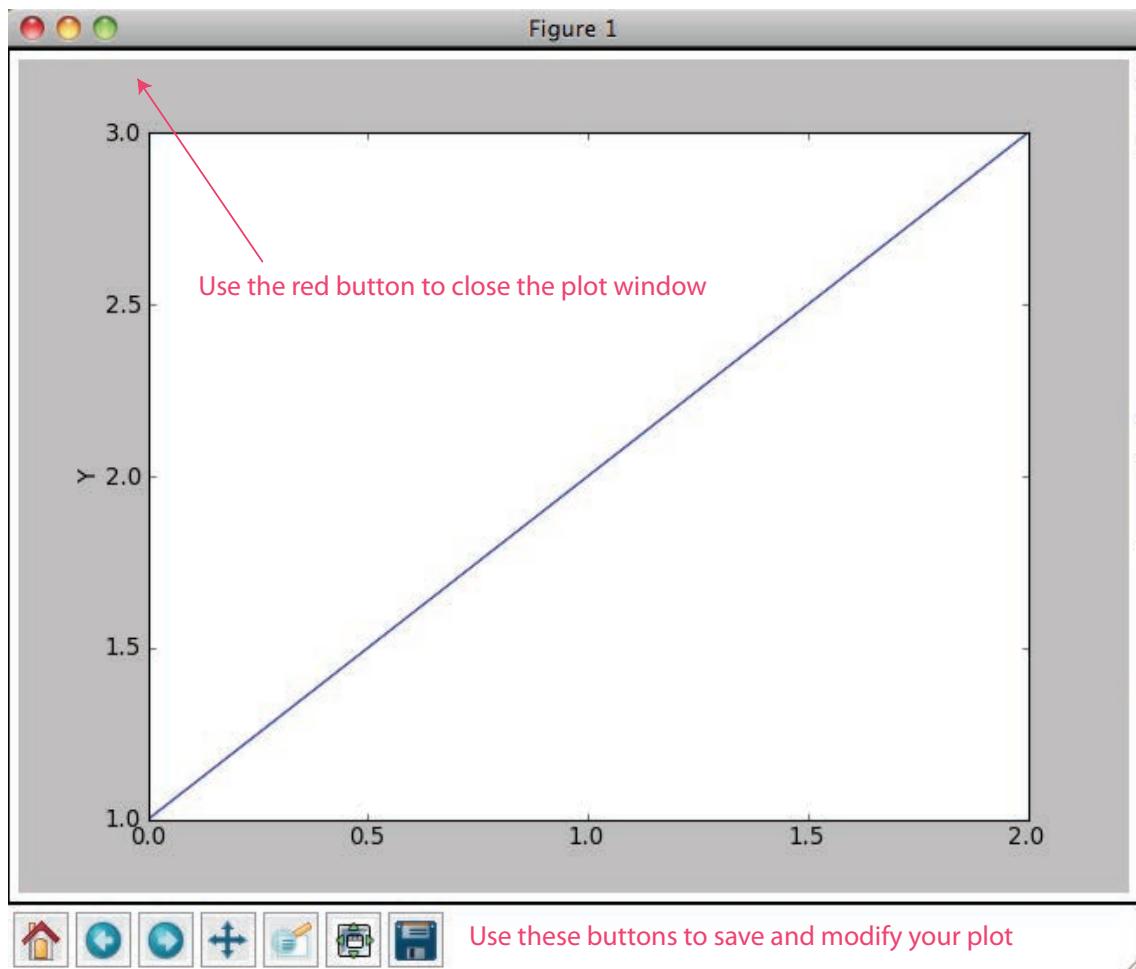
In the above example, we call the `plot` method with a list as an argument. As we mentioned, `matplotlib` uses the concept of “classes” to make plots and this has just happened behind the scenes. We could have named the plot instance with a the `figure()` method (e.g., `fig=pylab.figure()`) and then referred to it later with the command `fig.plot([1,2,3])`, but we don’t have to in this simple case - the class instance is implied and is the “current plot”. You can tell this, if you do the above example in interactive mode:

```
>>> import matplotlib
>>> matplotlib.use('TkAgg')
>>> import pylab
>>> pylab.plot([1,2,3])
[<matplotlib.lines.Line2D object at 0x4bd6eb0>]
```

The bit about `[<matplotlib.lines.Line2D object at 0x4bd6eb0>]` is Python’s way of telling you that you just created an object and something about it. In any case, when you give `plot()` a single sequence of values (as above), it assumes they are *y* values and supplies the *x* values for you.

Attributes of the `pylab` class, such as the Y axis label can be changes with the `ylabel` method. As you can imagine, there are LOTS of methods, including, surprise, an `xlabel` method.

When we are done customizing the plot instance, we can view it with the `show` method. When that gets executed, we will get a plot something like this:



Once that happens, we won't be able to change the plot any more and in fact, we won't get our terminal back until the little plot window is closed. You can save your plot with the little disk icon in a variety of formats. Adobe Illustrator likes .svg, or .eps while Microsoft products like .png file formats.

If you find it annoying to always have to close figures with the little red button, or save them with the disk icon, you can tweak the program like this:

```
#!/usr/bin/env python
import matplotlib
matplotlib.use('TkAgg')
import pylab
```

```

pylab.ion() # turn on interactivity
pylab.plot([1,2,3])
pylab.ylabel('Y')
pylab.draw() # draw the current plot
ans=raw_input('press [s] to save figure, any other key to quit: ')
if ans=='s':
    pylab.savefig('myfig.eps')

```

The method `pylab.savefig(FILENAME.FMT)`. The .FMT can be one of several, e.g., .eps, .svg, .ps, .pdf, .png, .gif, .jpg, etc.). Some of these (the vector graphics ones like pdf, ps, eps and svg) can be opened in Adobe Illustrator for modification.

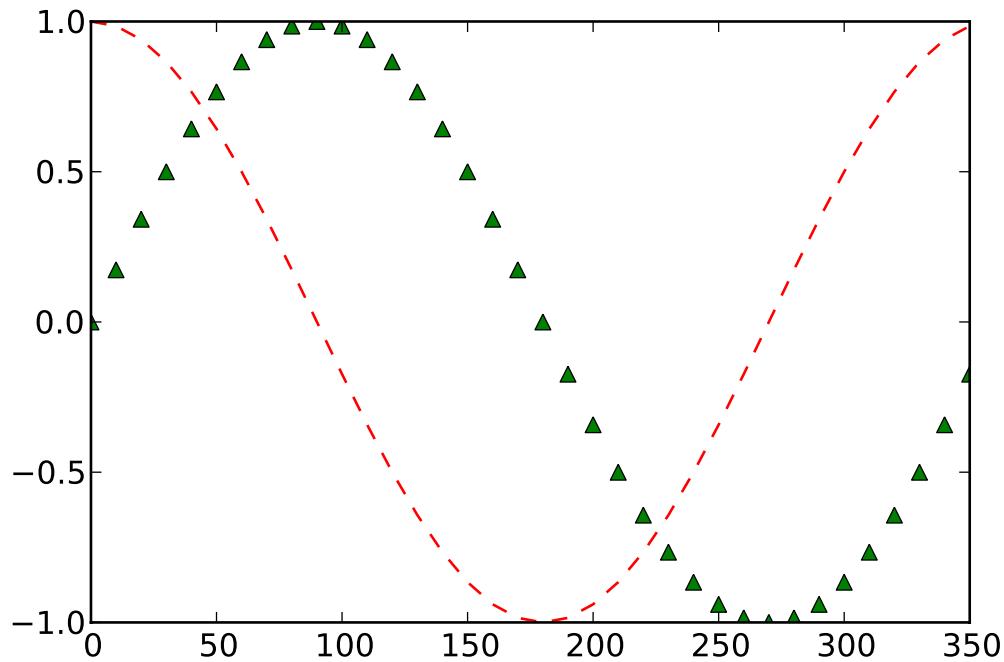
As mentioned earlier, if you give `plot()` a single sequence of values, it assumes they are y values and supplies the x values for you. Garbage in, garbage out. But `plot()` takes an arbitrary number of arguments of the form: $(X_1, Y_1, \text{line_style_1}, X_2, Y_2, \text{line_style_2}, \text{etc.})$, where 'line_style' is a string that specifies the line style as illustrated in this script called `matplotlib2.py`

```

#!/usr/bin/env python
import matplotlib
matplotlib.use('TkAgg')
import pylab, numpy
x=numpy.arange(0,360,10)
r=x*numpy.pi/180.
c=numpy.cos(r)
s=numpy.sin(r)
pylab.plot(x,c,'r--',x,s,'g^')
pylab.show()

```

which produces the plot:



From the code, you can probably figure out that a line style of 'r-' is a red dashed line, and 'g^' are green triangles. There are many other attributes that can be controlled: linewidth, dash style, etc. and we invite you to check out the [matplotlib](#) documentation.

By now, you should understand enough about classes, keyword argument passing and other pythonalia to be able to figure things out on your own. But don't panic, I'm going to lead you through a few more examples, which we hope will speed you on your plotting way.

Multiple figures and more customization

As already mentioned, `pylab` has the concept of “current figure” which subsequent commands refer to. In the preceding examples, we only had one figure, so we didn’t have to name it, but for fancier figures with several plots, we can create named figure objects by invoking a `figure` instance:

```
fig = pylab.figure(num=1, figsize=(5,7)).
```

Notice the syntax whereby `figsize` is a method with width and height (in inches) specified by a tuple and `num` is the figure number. Notice that these

are keyword arguments, and that there are many more: consult the list of `**kwargs` in the online documentation located here:

http://matplotlib.sourceforge.net/api/pyplot_api.html#matplotlib.pyplot.figure

Once we have a figure instance (sometimes called a “container”), we can do all kinds of things, including adding subplots. To do this, we can use the syntax:

```
fig.add_subplot(211)
```

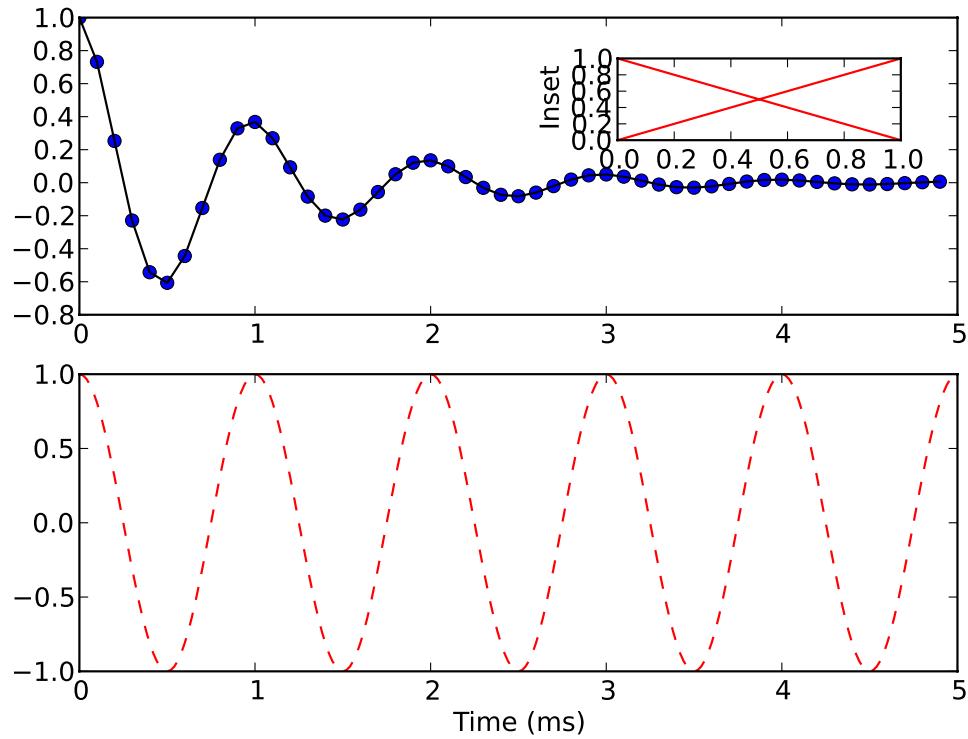
Here the argument 211 means 2 rows, one column and this is the first plot. To make plots side by side, you would use: `fig.add_subplot(121)` for 1 row, two columns, etc.

After each `add_subplot` command, that subplot becomes the current figure for plotting on. If you want more freedom, say, you want to make a subplot at an arbitrary place, use the `add_axes([left, bottom, width, height])` method, e.g., `add_axes([0.1,0.1,0.7,0.3])`. The values are 0-1 in relative figure coordinates.

To illustrate these new concepts, consider the example code, `matplotlib3.py`:

```
#!/usr/bin/env python
import matplotlib
matplotlib.use('TkAgg')
import pylab, numpy
def f(t):
    return numpy.exp(-t)*numpy.cos(2.*numpy.pi*t)
t1= numpy.arange(0.,5.,0.1)
t2= numpy.arange(0.,5.,0.02)
fig=pylab.figure(num=1,figsize=(7,5))
fig.add_subplot(211)
pylab.plot(t1,f(t1),'bo')
pylab.plot(t1,f(t1),'k-')
fig.add_subplot(212)
pylab.plot(t2,numpy.cos(2*numpy.pi*t2),'r--')
pylab.xlabel('Time (ms)')
fig.add_axes([.6,.75,.25,.10])
pylab.plot([0,1],[0,1],'r',[0,1],[1,0],'r')
pylab.ylabel('Inset')
pylab.show()
```

which produces:



By now, you should be able to figure out what everything in that script does by yourself!

Adding text

We already met `xlabel` and `ylabel`. But text can be added in other ways, e.g., using the `title`, `text`, `legend` and `arrow` methods. Let's decorate one of our early examples to show how some of these things work:

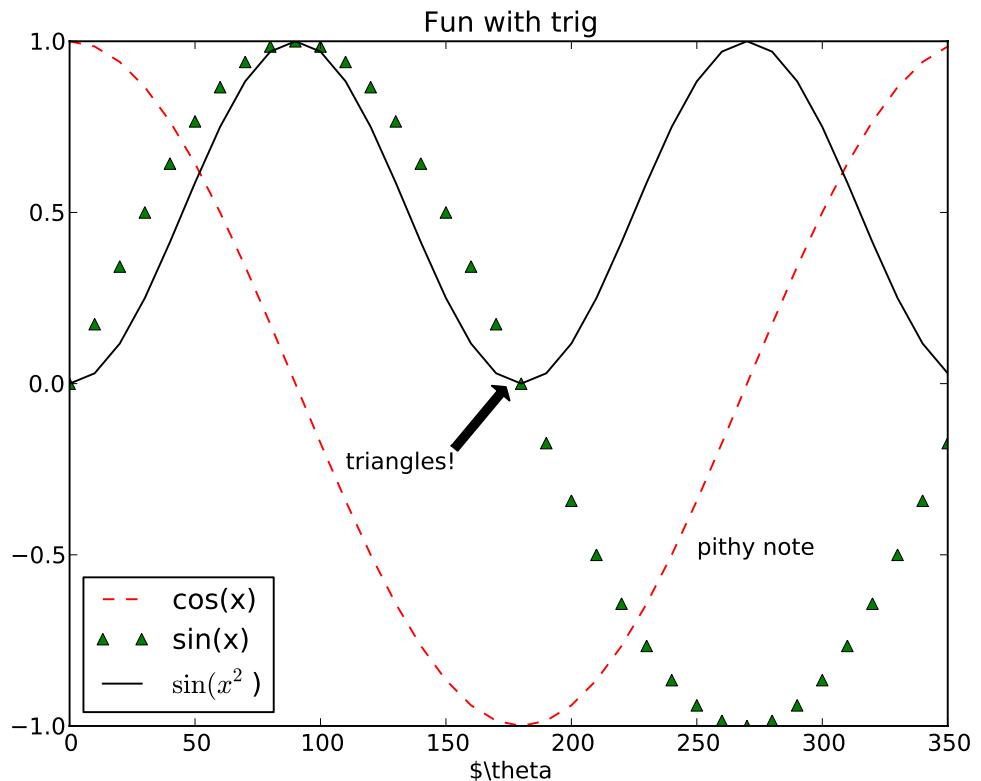
```
#!/usr/bin/env python
import matplotlib
matplotlib.use('TkAgg')
import pylab, numpy
x=numpy.arange(0,360,10)
r=x*numpy.pi/180.
c=numpy.cos(r)
```

```

s=numpy.sin(r)
s2=numpy.sin(r)**2
pylab.plot(x,c,'r--',x,s,'g^',x,s2,'k-')
pylab.title('Fun with trig')
pylab.text(250,-.5,'pithy note')
pylab.legend(['cos(x)',\
    'sin(x)',r'$\sin(x^2)$'], 'lower left')
pylab.xlabel(r'$\theta$')
pylab.annotate('triangles!',\
    xy=(175,0),xytext=(110,-.25),\
    arrowprops=dict(facecolor='black',\
        shrink=0.05))
pylab.show()

```

which produces this plot:



The title appears at the top of the plot. Text labels get places at the x

and y coordinates on the plot and the legend will appear in the upper/lower right/left corner as specified in the string. The `pylab.text(x,y,string, kwargs)` method also has optional key word arguments, specifying font, size, color and the like. The legend 'labelist' is a list of labels for each plot element. So, every line or point style that you want in your legend, append a label to the label list after the relevant plot command. Also note that the legend and xlabel methods use a special format for strings (`r'LateX String'`) which allows embedded LaTeX equation syntax to make scientific equations look right - so now you have to learn LaTeX!. Finally, the arrow gets drawn with the `annotate` method, which has a lot of other attributes as well. Check the `matplotlib` documentation for details.

There are lots of graphing styles possible with `matplotlib`, e.g., histograms, pie charts, contour plots, whisker plots, etc. I'm just going to show you a few examples. The best thing to do is to look through the online documentation for a plot that looks like what you need, then modify it. This is ALWAYS a good approach - start with something that works and fiddle with it until it suits your own particular needs.

Chapter 8

Jupyter Notebooks

Data analysis in Python benefits from an increasingly robust ecosystem of packages for scientific computing and plotting. A tool that has gained increasingly widespread use for conducting and presenting data analysis is the Jupyter notebook. The Jupyter notebook builds on the IPython project which began as a way to bring increased interactivity to data analysis in Python (Pérez & Granger, 2007) and has evolved to include an interactive notebook environment that seeks to enable the full trajectory of scientific computing from initial analysis and visualization onwards to collaboration and through to publication. The project has expanded to enable a reproducible interactive computing environment for many other programming languages (such as R and Julia) and the language-agnostic parts of its architecture have recently been rebranded as Project Jupyter (<http://jupyter.org>). Jupyter notebooks allow for executable code, results, text and graphical output to coherently coexist in a single document. With these combined components, they are excellent tools both for conducting data analysis and presenting results.

Underlying the **PmagPy** programs that are accessible through the command line and the GUI interfaces (e.g., **Pmag GUI**) are two main function libraries: **pmag.py** and **pmagplotlib.py**. The functions within these modules can be imported and called upon within a Jupyter notebook running a Python 2.7 kernel. In addition to these functions, Nick Swanson-Hysell created a module called **ipmag.py** that is in active development and contains functions that replicate and extend functionality that is found within the **PmagPy** command line programs for use in the notebook environment.

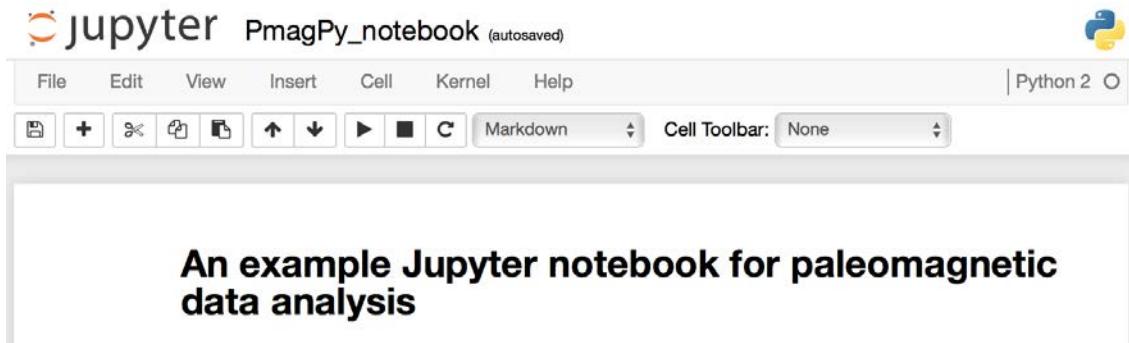
To show some of what is possible in terms of data analysis using **PmagPy** in a notebook environment, we have created example notebooks that are

available for download from this repository: https://github.com/PmagPy/2016_Tauxe-et-al_PmagPy_Notebooks.ipynb. These notebooks can also be viewed as static webpages here: http://pmagpy.github.io/Example_Notebooks.html and http://pmagpy.github.io/Additional_PmagPy_Examples.html.

The main example notebook (`Example_PmagPy_Notebook.ipynb`) combines data from two different studies for the sake of developing a mean paleomagnetic pole from the upper portion of a sequence of volcanics in the North American Midcontinent Rift (?*Swanson-Hysell et al.*, 2014). The two data files used within the notebook can be downloaded from the MagIC database. The digital object identifier (doi) search option allows for the data files to be readily located as <https://earthref.org/MagIC/doi/10.1139/e74-113/> and <https://earthref.org/MagIC/doi/10.1002/2013GC005180/>. Downloading these data files from the database and putting them into folders within a local ‘Project Directory’ allows them to be accessed within the Jupyter notebook. Within the notebook, these data are unpacked into their respective MagIC formatted tab delimited data files. The data are then loaded into dataframes and filtered using several different criteria (stratigraphic height and polarity). Several functions from the `ipmag` module are used for making equal area projections and calculating statistics. In addition to combining the data sets to calculate the mean pole, the code in the notebook conducts a bootstrap fold test on the data using the approach of Tauxe & Watson (1994) as well as a common mean test. The data recombinations and calculations done in this notebook are examples of portions of the data analysis workflow which are often difficult to document and reproduce. The examples illustrate a small sliver of the potential for the use of notebooks for data manipulation and analysis of paleomagnetic data. Additional functionality available within PmagPy is demonstrated within the additional **PmagPy** examples notebook (`Additional_PmagPy_Examples.ipynb`) as small vignettes of example code. Functions related to paleomagnetic and rock magnetic data analysis are shown as examples. The notebook also illustrates some of the interactivity that can be built into the notebook utilizing IPython widgets.

To execute and edit notebook code yourself, you can clone or download this repository: https://github.com/PmagPy/2016_Tauxe-et-al_PmagPy_Notebooks. If you installed the Enthought Canopy or Anaconda Python distribution you will have the IPython and Jupyter packages installed. If you have another Python distribution you will want to make sure that you have IPython and Jupyter (installation instructions can currently be found here: <http://ipython.org/install.html> and here: <http://jupyter.readthedocs.org/en/latest>). To view and edit the notebooks, type **ipython notebook** or **jupyter notebook** on the command line. This command will open up a local IPython

server in your default web browser within which you can use the directory to navigate to the data_files folder. Click on it to open and edit. You will see something like this:



Notebooks are constructed as a series of ‘cells’ which can be text or code. To view the ‘source’ of a text cell, just click on it. To render it, click on the ‘run’ button (sideways triangle on the toolbar). Similarly, to run the code in a code cell, click on the cell and then the ‘run’ button (or use the shift+enter short cut). To execute the entire notebook, click on the ‘Cell’ button and choose ‘Run All’.

To use **PmagPy** within the notebook, the **PmagPy** function modules need to be in your Python path. This . There are two ways to do this. One way is to have your .profile or .bash_profile have a line in it that reads :

```
PYTHONPATH=$PYTHONPATH:/PmagPy
```

Another way is to set the path to the location of your PmagPy folder within the notebook itself. The default location on MacOS is in a folder called *PmagPy* in your home directory (e.g., /Users/YOUR_NAME_HERE/PmagPy) and on Windows is in the Documents folder (e.g., 'C:

Users

YOUR_NAME_HERE

Documents

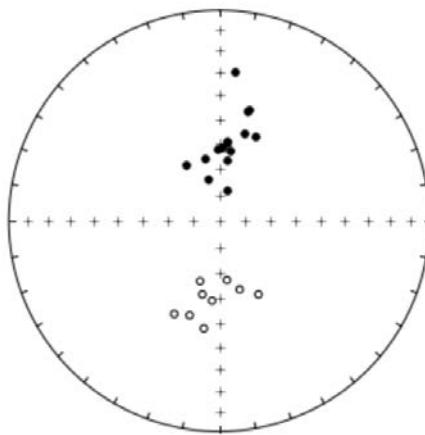
PmagPy

PmagPy’. To do this you must `import os` and then have a line that reads `sys.path.insert(0, '/Users/.....')` where the path reflects your own path. If PmagPy is in your path you should be able to run the first code block which imports the **PmagPy** modules and makes them available available to use within the notebook. The notebooks also import several other Python modules useful for scientific computing (numpy), data manipulation (pandas) and plotting (matplotlib).

Now you are ready to look at some data. In the code block under the heading ‘Reading data from MagIC format results files’, data are read in from a file downloaded and unpacked from the MagIC database. The notebook shows how to read in the data into a pandas DataFrame, and plot the directions on an equal area projection:

```
In [6]: fignum = 1
plt.figure(num=fignum, figsize=(6, 6), dpi=160)
ipmag.plot_net(fignum)
plt.title('Snake River Plain site mean equal area plot')
ipmag.plot_di(DI_results['average_dec'], DI_results['average_inc'])
```

Snake River Plain site mean equal area plot



There are several other tricks shown off in the notebook, which should be enough to get you started using **ipmag** in a Python notebook environment. Conducting data analysis using **PmagPy** in a notebook allows for the underlying code of statistical tests to be available and for the decisions made in the specific implementation of such tests to be transparently presented.

Although there is much much more to do in Python, this documentation is aimed at getting and using **PmagPy**, so that’s it for this chapter. Congratulations if you made it to the end!

Chapter 9

Troubleshooting

9.1 Problems with installing Python or PmagPy

1. Nothing works as advertised!

- First, please test that you have successfully installed the appropriate Python distribution.
- For Mac users, find your command line (Terminal) and type “python”. You should see something like this:

```
$ python
Enthought Canopy Python 2.7.6 | 64-bit | (default, Jun 4 2014, 16:42:26)
[GCC 4.2.1 (Apple Inc. build 5666) (dot 3)] on darwin
Type "help", "copyright", "credits" or "license" for more information.
>>>
```

- For windows users, find your command line (Command Prompt), and type “python”. You should see something like this:

```
$ python
Enthought Python Distribution -- www.enthought.com
Version: 7.3-2 (32-bit)

Python 2.7.3 |EPD 7.3-2 (32-bit)| (default, Apr 12 2012, 11:28:34)
[GCC 4.0.1 (Apple Inc. build 5493)] on darwin
Type ``credits``, ``demo`` or ``enthought`` for more information.
>>>
```

- If you don't see one of the above messages, you have not fully installed the Python distribution. You'll need to try again. For Mac users, in order to complete the install you must start Canopy (it will be in Applications) and select "yes" to use Canopy Python as your default Python. For Windows users, you should be prompted during the install process to make Enthought Python your default Python, and you need to select yes.
2. I've installed the proper Python distribution, but PmagPy doesn't work

- For Mac users:

When you try to run eqarea.py -h to test your installation, you get this error message:

```
-bash: eqarea.py: command not found
```

There are a few possible reasons for this failure, the most common of which is that your path has not been correctly set. To test this, type "echo \$PATH" in your command line.

You will see something like this:

```
/Users/****/Library/Enthought/Canopy_64bit/User/bin: /usr/local/bin:  
/usr/local/share/npm/bin: /usr/bin: /bin: /usr/sbin: /sbin:  
/usr/local/bin: /opt/X11/bin: /Users/****/PmagPy:/usr/texbin
```

Your \$PATH may look very different, but as long as you have the complete path to the PmagPy directory in there, you are golden. If the directory is not in your path, you can try re-running the PmagPy install script, which should set your path correctly for you. If that doesn't work, go to your home directory (to get there, type "cd" in your command line). Use a text editor to open a file called .bash_profile and add these lines:

```
export PATH=/Users/***/PmagPy:$PATH  
export PATH=/Users/***/PmagPy/programs:$PATH  
export PYTHONPATH=$PYTHONPATH:/Users/***/PmagPy/
```

where *** is your username. Then restart your Terminal. If it still doesn't work, see question 3.

- For Windows users:

```
"eqarea.py" is not recognized as an internal or external command,  
operable program or batch file.
```

Setting your path should not be an issue in Windows if you are using the PmagPy prompt (created by the install script). PmagPy functionality will be available only in the custom Command Prompt, so make sure you are using it. However, if you do need to set your path for some reason, see:

Setting your Path in Windows

If you are using the pip install instead of the PmagPy prompt, you'll need to use the command "eqarea -h", **not** "eqarea.py -h". This is caused by a strange Windows quirk, but all you need to know is this: anytime the Cookbook gives a command, you'll need to drop the ".py" and all will be well.

3. My path is correctly set, but I still get this error message:

```
-bash: eqarea.py: command not found
```

- For Mac users, it is possible that you need to make the python scripts executable. On the command line in the directory with the scripts, type: chmod a+x *.py

9.2 Problems updating Canopy

If you are using Canopy (not just EPD), you will need to keep it up to date. Currently, that means the version number should be 1.6.1 or higher. In general, you can update by opening the Canopy application; it will automatically check for updates. However, if you haven't updated for a long time, Canopy can get "stuck" in an old version where it can no longer update. If that is the case, you will need to fully uninstall and reinstall canopy, following the directions on the Enthought website.

9.3 Problems with a specific program

1. Thellier auto_interpreter crashes with a Segmentation Fault (on Mac).
 - This error is caused by a version issue with one of PmagPy's dependencies, matplotlib. There are two ways to solve this problem.

- Recommended: download and use the standalone Pmag GUI distribution to access Thellier GUI.
- Alternative: open the Canopy application, and navigate to the Canopy Package Manager. Go to “Installed packages” and find matplotlib. Click matplotlib’s “more info” button. The click “show” to see all versions of the package. Select matplotlib 1.4.3-7 and install. This will fix the segmentation error, however, it may cause the Thellier GUI menubar to behave oddly. For this reason, we recommend the first solution (above).

9.4 Other problems

Report a problem not listed above: e-mail ltauxe@ucsd.edu. Include the following information: 1) the version of PmagPy that you are using, 2) your operating system, 3) any error messages that you got, 4) the datafile that is giving trouble, if relevant.

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